APPENDIX A

| | | | | | | | | | | | | | • | | | | | • | 7 | | | | | | | | | | | | | | | | |
|----------|---|----------|----------------------------------|---------------------------------|----------------|----------------------------------|----------------------|----------------|----------------------|--------------------------------|----------------|--|---|--|--|--------------------------------------|--|--------------------------------------|------------------------------------|--|--------------|-------------------|---------------|---------------------|--------------------|--------------------------------------|---------------------------------|--------------------|--|------------------|------------------|---|--|--------------------------------|------|
| | 100 M | | | | | | | | | | | | NS and | tuitary, | testine, | testes. | יטטי :סטי ייין ייין | Aldiley. | | ystem, | | | | | | | | o io io | | poorly. | | poorly | | | |
| | | | | | | | | | | | , | nesis | generating: Released by hepatic nerves; CNS and | glucose peripheral organs including pituitary. | hepatic pancreas, small and large intestine, | adrenal gland, lung, tongue, testes. | ovary-fallopian tubes, and uterus; not | detectable in neart, liver, kiulley. | urinary bladder or skeletal muscle | ceramide. CNS and peripheral nervous system, | distribution | | | | | | | And Contact Allega | Brain; tissue distribution and protein poorly characterized | expression | | distribution | | | |
| 9 | | 18 | | | | | | | | | | Semaphorin F; involved in axonal Early embryogenesis | ed by he | eral orga | as, sma | l gland, | fallopian | able . in | , bladder | ind perip | | terized | | | | | | , | Brain; tissue distrible populy characterized | 6 | characterized | Bpx, strong homology to genes Brain; tissue | terized | | |
| Location | | n Neuror | | > ' | = | 9 | | - CNS | 0 | s | | al Early e | . Releas | e pariph | c pancre | adrena | ovary. | detect | urinary | - CNS | key tissue | and characterized | :: | = | | O Brain | 0 | | Brain; | s Brain; | charac | s Brain; | y charac | | |
| | | 1 protei | proteil | 643 ma | sing of | in to th | | outgrowth- CNS | guidance | ng axon | | in axon | opentide | alucos | hepati | • | | | | ceramide | | | biosynthesis; | most | ; | 7-7); +17 | binds t | | | anonymous Brain; | | to gene | assembl | rized | |
| | STIIS STU | ine; X1 | binds amyloid precursor protein, | receptor trafficking; +1543 may | the processing | amyloid precursor protein to the | ptide | | <u>:</u> | molecule; guides growing axons | , | nvolved | | pat | present in | | | | | | transferase; | cerebroside | | ds; | rile | Neurexophilin 2 (Nxph-2); +120 Brain | neuronal glycoprotein; binds to | | 27 | | | mology | encoding nucleosome assembly characterized | proteins; poorly characterized | |
| | ERVOU | otein ge | myloid | r traffic | the | precurs | amyloid beta peptide | XB | _ | e; guide | in development | iorin F; i | | | ë | | | | | lactose | _ | .⊆ | 6 0 | glycosphingolipids; | abundant in myelin | philin | l glycol | alpha-neurexins | Sodium channel 27 | expressed | | rong ho | g nucle | ;; poorly | |
| | Descrip | X11 pr | binds a | recepto | regulate | amyloid | amyloid | Netrin-1: | promoting | molecul | in devel | Semaph | guidance | onhances | production; | nerves | | | | UDP-galactose | galactosyl | enzyme | sulfatide | glycosp | apnuqa | Neurex | neurona | alpha-n | Sodium | cia:a | ANO. | Bpx, st | encodin | proteins | -63- |
| | P CR std CON std SW std GenBank Description | L34676 | | | | | | 1165418 |) | | | X97817 | | 138580 | | | | | | X92122 | | | | | | 056650 | | | L42340 | V61440 | 2 | X92352 | | | |
| | Std | 0.18 | | | | | | 110 | <u>-</u> | | | 0.19 | | 0.03 | | | | | | 0.16 | | | | | | 0.18 | | | 90.0 | ; | <u>-</u> | 0.20 | | | |
| | SW | 1.20 | | | | | | 1 23 | 7. | | | 1.09 | | 1.06 | | | | | | 1.14 | | | | | | 1.16 | | | 1.04 | | = | 7 | | | |
| | Std | 0.00 | - | | | | | 70 0 | 7.6 | | | 0.00 | | 0.08 | | | | | | 0.03 | | | | | | 0.10 | } | | 90.0 | 0 | 0.0 | 000 | | | |
| | CON | 0.00 | | | | | | 9 | 0.20 | | | 00.00 | | 0.0 | | | | | | 0.02 | | | | | | 0.06 | | | 0.04 | | 0.03 | 5 | 5 | | |
| | Std | 0.79 | | | | | | , | 0.7/ | | | 0.02 | | 0.0 | | | | | | 0.16 | ; | | | | | 0.10 | 2 | | 0.22 | | 0.27 | , | - - - | | |
| | CR | 0.88 | | | | | | i. | C. 33 | | | 10 | : | 1.02 | | | | | | 1 14 | : | | | | | 10 | 2 | | 0.99 | | 1.16 | | 2 | | |
| | P | 0.046 |) | | | | | 6 | 0.006 0.95 0.27 0.28 | | | 70.001 1.10 0.02 | - - - - | <0.001 1.02 0.01 | | | | | | ZO 001 1 14 0:16 0:02 | | | | | | 1 10 0 10 0 00 | 0.00 | | <0.001 0.99 0.22 | | <0.001 1.16 0.27 | 0 | <0.00 1:13 0:05 0.00 21:10 0:05 | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

| Location PLP; proteolipid protein, main CNS integral protein of the myelin Glutamic acid decarboxylase 67 Brain, islets: isozyme of liver form Glutamic acid decarboxylase 67 Brain, islets: isozyme of liver form Glutamic acid decarboxylase 67 Brain, islets: isozyme of liver form KD. Cadherin-8, adhesion molecule MCad8 expression is restricted to Cadherin-8, adhesion molecule central nervous system (CNS) and to | the thymus Inward rectifier potassium Neurons channel 2 (GIRK2) K+ channel beta-subunit, ion Brain and Kidney channel | SNS-TTXi sodium chainter, by SNS-TTXi sodium chainter, by Channel; small-diameter sensory channel; small-diameter sensory neurons associated with neurons express a unmyelinated axons express a tetrodotoxin-insensitive (TTXi) tetrodotoxin-insensitive (TTXi) charge-gated sodium channel (VGSC); may play an important role in the transmission of nociceptive information to the | spinal cord Potassium channel gene (MK2); T cells; myelinating Schwann (:ells Shaker subfamily Any change homeobox gene (NKx- Developing CNS and ear in £13.5 | 6.2); cell type specification of embryos; cell type specification of embryos; cell type specification of embryos; cell surface heparin in embryo major sitos are tubular K-dypican; cell surface heparin in embryo major sitos and | sulfate proteoglycan; suggested epithelial cells in roll in regulating cell cycle proliferating neuroepithelial cells in progression during the transition brain; neurons of neural cells from proliferation | |
|--|---|---|---|--|--|--------------------------|
| GenBank X07215 Y12257 ET63017 | ET61642 X97281 | Y09108 | M30440 | 580989 | 2000 | U36757 |
| std 0.22 0.25 0.35 | 0.12 | 0.08 | 0.39 | | 0.13 | 0.28 |
| SW 1.22 1.16 | 1.43 | | | 1.10 | 0.24 1.22 | 1.32 |
| std 0.05 0.06 0.00 | 0.15 | 0.12 | 0.26 | 0.46 | 0.24 | 1,12 0.26 0.61 0.27 1.32 |
| | 0.09 | 0.10 | 0.15 | 0.40 | 1.00 0.21 0.50 | 0.61 |
| std C 0.29 C 0.19 C | 0.35 | 0.07 | 1.26 0.03 | 0.50 | 0.21 | 0.26 |
| CR std CON 1.29 0.29 0.03 1.17 0.19 0.03 1.36 0.15 0.00 | 1.19 0.35 | 1.06 | 1.26 | 1.78 | | 1.12 |
| P CR 0.001 1.29 <0.001 1.17 0.001 1.36 | 0.001 | <0.001 1.06 0.07 0.10 | 0.005 | 0.018 | 0.011 | 0.044 |

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| Description serine protease generated by the activation of the blood coagulation cascade following vessel injury; thrombin acts as a mitogen, apoptosis inducer and regulator of inflammation Dilute lethal-20J; Class-V Adult germ line cells; early embryo; myosin; unique type of myosin oocyte during oogenesis; enriched in | motor; role in vesicular brain; neurons; melanocytes menotor; role in vesicular brain; neurons; melanocytes membrane traffic through actin rich regions of the cytoplasm; transport endoplasmic reticulum vesicles in neurons and pigment granules in melanocytes receptor 8 lymphocytes; dendritic cells. | recept es; de cells. ie Dros p | functioning in neural development. Connexin30 (CX30); gap junction Brain; skin protein that forms transmembranous gap junction | | Neurotrophin-3 (NT-3); secreted Liver parenchymal cells ollactory protein; binds high affinity bulb cerebellum; septum and hippocampus; thymus, heart, diaphragm, pancreas, spleen, kidney. adrenal gland |
|---|--|--|--|-----------|---|
| GenBank | ET62839 | ET63156 | ET63385 | ET63410 | X53257 |
| std 0.12 | 0.06 | 0.55 | 0.36 | 0.38 | 0.21 |
| sw | 0.98 | 1.36 | 1.37 | 1.40 | 1.12 |
| std | 000 | 0.20 | 0.09 | 0.56 | 0.15 |
| CON 0.53 | 0000 | 0.20 | 0.05 | 0.43 0.33 | 0.09 |
| std 0.02 | 90 | 1.14 0.15 | 1.21 0.21 | 0.43 | 0.0 |
| CB 1.02 | 2 | 1.14 | 1.21 | 1.44 | 1.12 |
| P CR std CON | C | | 0.001 | 0.043 | <0.001 1.12 0.04 0.09 |

-65-

| Location Discs-large tumor suppressor Localized to synapse; epithelial cells biscs-large tumor suppressor Localized to synapse; epithelial cells homologue (dlgh1); important role in the localization and function of glutamate receptors and K(+) channels; member of the MAGUK (membrane associated guanylate kinase homologue) family of | proteins Axonemal dynein heavy chain Brain, trachea, testis (mdhc1); axonemal dyneins are molecular motors that drive the beating of cilia and flagella; heavy chains are main components of multisubunit motor ATPase complexes called | dyneins Axonemal dynein heavy chain Brain, trachea, testis (mdhc3); axonemal dyneins are molecular motors that drive the beating of cilia and flagella; heavy chains are main components of multisubunit motor ATPase complexes called | dyneins Axonemal dynein heavy chain Brain, trachea, testis (mdhc6); axonemal dyneins are molecular motors that drive the beating of cilia and flagella; heavy chains are main components of multisubunit motor ATPase complexes called | Axonemal dynein heavy chain Brain, trachea, testis Axonemal dyneins are (mdhc9); axonemal dyneins are molecular motors that drive the beating of cilia and flagella; heavy chains are main -66- |
|--|---|--|--|---|
| GenBank ET61665 | ET63395 | £763399 | ET63402 | ET63405 |
| std 0.19 | 0.15 | 0.0 | 1.30 0.42 | 0.23 |
| sw 1.22 | 1.32 | | | 4.1 |
| std 0.26 | 0.27 | 0.00 | 0.36 | 0.21 |
| 0.22 | 0.16 | 1.21 0.17 0.00 | 0.21 | 1.07 0.09 0.24 |
| std 0.28 | 0.20 | 0.17 | 0.08 | 0.0 |
| CR 1.16 | 1.05 0.20 0.16 | 1.21 | 1.09 | |
| P.0004 | 0.001 | 0 | 0.013 | 0.002 |

| Description Location components of multisubunit motor ATPase complexes called | dyneins Synaptonemal complex protein 3; Testis; synaptonemal complex Synaptonemal complex; a embryonic ovary, adult brain and synaptonemal complex; a embryonic ovary, adult brain and meiosis-specific protein structure testis essential for synapsis of | homologous chromosomes Gonadotropin-releasing hormone Anterior pituitary, brain and Gonadotropin-releasing hormone Anterior pituitary, brain receptor; G-protein-coupled reproductive organs as well as many receptor; GnRH activates all four steroid-dependent tumor tissues MAPK cascades by a PKC- | dependent mechanism. Preproglucagon; glucagon-like Pancreatic alpha cells, ileum + K41. peptide I and !I; member of CNS vasoactive intestinal peptide (VIPI/secretin/glucagon/GHRH | family of neuropeptides Fibroblast growth factor Highest expression in brain and Fibroblast growth (FGF-1); skeletal muscle nervous system development and | function Relaxin precursor (rlx); relaxin; Brain, uterus, prostate gland, member of insulin gene family; pancreas and kidney, with other remodeling of collagen and tissues giving weak signals | uterine contractuity Ankyrin-3 (Ank3); also called Widely distributed, especially in Ankyrin(G); skeletal protein epithelial tissues, muscle, and implicated in Na(+) channel neuronal axons clustering; essential for clustering NaCh and neurofascin axon initial segments and is required for the channel axon contraction initial segments and is required to the contraction of | |
|---|--|--|--|--|---|--|----------------------|
| GenBank | Y08485 | L28756 | 246845 | U66201 | 227088 | ET62740 | U48397 |
| std | 0.08 | 0.30 | 0.10 | 0.15 | 0.18 | 0.29 | 0.25 |
| S. | 1.34 | 1.28 | 1.09 | 1.10 0.15 | 0.99 | 0.22 1.23 | 0,35 1.05 |
| std | 0.09 1,14 | 0.00 1.28 | 0.23 | 0.11 | 0.00 | 0.22 | 0.35 |
| CON | 1.02 0.08 0.05 | 0.00 | 1.18 0.24 0.29 | 0.08 | 0.00 | 1.20 0.24 0.25 | 0.007 1.37 0.08 0.34 |
| std | 0.08 | 0.53 | 0.24 | 0.15 | 0.15 | 0.24 | 0.08 |
| CB | 1.02 | 1.20 | | 1.09 | 1.13 | 1.20 | 1.37 |
| Q. | 0 | 0.007 1.20 0.53 0.00 | 0.003 | <0.001 1.09 0.15 0.08 | <0.001 1.13 0.15 0.00 | 0.005 | 0.007 |

-67-

| Description Location water and small solutes to pass | Discs-large tumor suppressor Localized to synapse, ejunicular componentalism gene; homologue (dight) gene; important role in the localization | and function of glutamate receptors and K(+) channels; member of the MAGUK (membrane associated guanylate rinase homologue ues) family of | proteins pro | Neuropeptide Y receptor Neurons, vascular smooth indecidents $\gamma_5\gamma_6/\gamma_2b$ (referred to as both cells | Y5 and Y2b, has now been designated as Y6 in literature); (NPY-Y6); neuropeptide Y is an important regulator of energy balance in mammals through its norexinentic, antithermogenic, and | insulin secretagogue actions; expressed abundantly in the central nervous system; NPY receptors mediate a variety of | physiological responses incremes feeding and vasoconstriction receptor type-3; Skeletal and smooth muscle, CNS hypomoting C2+ channels | Neosin/lark; RNA-binding protein; Uncharacterized, probably neuronal Drosophila for the choosing of the chock output | an elativation of the colorion of the colorion (circadian rhythm) Histamine H1 receptor; GTP- Liver, brain, spleen (ubiquitous) binding protein-coupled receptor; coupled to phosphoinositide turnover-calcium mobilization |
|--|---|---|--|--|--|---|--|--|---|
| GenBank | ET61665 | | M30440 | U58367 | | | ET61090 | ET62978 | D50095 |
| std | 0.19 | | 0.39 | 0.10 | | | 0.37 | 0.10 | 0.27 |
| SW | 1.22 | • | 1.16 | 1.15 | - | | 1.56 | 1.10 | 1.18 |
| std | 0.26 | - | 0.26 | 0.03 | • | | 0.00 | 0.32 | 0.00 |
| CON | 0.22 | | 1.26 0.03 0.15 | 1.00 0.15 0.02 | | | 0.00 | 0.18 | 0.00 |
| std | 0.28 | | 0.03 | 0.15 | | | 0.15 | 0.24 | 0.31 |
| င္မ | 1.16 | | 1.26 | 1.00 | | | 1.06 | 96.0 | 1.24 |
| ۵ | 0.004 | | 0.005 | 0 | | | 0.000 1.06 0.15 | 0.006 | 0.001 1.24 0.31 0.00 |

| 5 | broad on | Activin type IB receptor; limb Embryo: brain, some ganglia, development; expressed vibrissae, lungs, body wall, stomach, coincidently with the formation gonads, ribs, limbs, shoulders, of the last phalanx of each digit offactory region, eye, tooth, primordium, esophagus, mesonephros, dorsal root ganglia and is strongly expressed in the spinal cond. | and paractine and paractine prevents cell ad motoneurons; embryonic neural differentiation; citivity (acts on proliferation of | (7:1) | Skeletal muscle-specific calpain Skeletal muscle; differentially spliced (canp3); intracellular calcium variants in smooth muscles during |
|-------------|----------------|--|---|--|---|
| GenBank | U60330 | 231663 | U33535 | (2017年) (1017年) (10 | X92523 |
| std | 0.13 | 0.18 | 91.0 | 0.13 | 0.39 |
| % `. | 1.15 | 1,18 | 1.31 | 1.04 | 0.80 |
| std. | 0.00 | 0.00 | 00.00 | SPIE 27 | 0.00 |
| N O O | 00.00 | 0.00 | 0.0 | 0.27 | 0.002 1.32 0.20 0.00 0.00 0.80 0.39 |
| std | 1.09 0.16 0.00 | 1.09 0.16 0.00 | 1.02 0.35 0.00 | PORTEINEIVERBINI 1.27 0.33 0.27 | 0.20 |
| S. | 1.09 | 1.09 | | 1.27 | 1.32 |
| œ. | 0 | 0 | 0.001 | GNOT-FREPORT-IN-ELVER3MUSEVIER 2017 1.04 0.13 0.07 0.08 1.27 0.33 0.27 0.27 1.04 0.13 | 0.002 |

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| | | | cooler box | Skeletal, cardiac muscie, and spicer. in adult | muscle | | | | | and cardiac muscle | , especially muscle, a |
|--|---|---|--|---|---|-------------------|----------------------------|--|---|--------------------|--|
| Description dependant cysteine proteinase; fetal period tissue specific myofibrogenesis, | modifies ryanodine receptor Ca2 + release channel Fibroblast growth factor (Fgf6); Skeletal muscle Fgf6 is the only known member of the FGF family whose expression is restricted to the muscle cell lineage during | development Nicotinic acetylcholine receptor Skeletal muscle beta subunit | Nicotinic acetylcholine receptor e Skeletal muscle subunit; embryonic | ZT3 zinc finger factor Skeletal, cardiac r | Protein phosphatase 2A Skeletal and heart muscle requiatory subunit | ily of giant s | annel anodine hannel | Dystrobrevin:postsynaptic Skeletal muscle protein; important in the formation and maintenance of the mammalian neuromuscular | ntegrin; a n involved in r matrix and | | Ankyrin-3 (Ank3); also called Widely distributed, ankyrin(G); skeletal muscle epithelial tissues, protein implicated in Na(+) neuronal axons |
| GenBank | M92416 | M14537 | X55718 | 267747 | . 037353 | ET62103 | ET62883 ET63019 | ET62998 | ET62865 | U49393 | ET62740 |
| std | 0.15 | 0.67 | 0.31 | 0.47 | 0.62 | 0.14 | 0.22 | 0.23 | 0.20 | 0.05 | 0.29 |
| SW | 1.17 | 1.45 | 1.11 | 1.19 | 1.29 | 1.14 | 1.14 | 1.27 | 1.21 | 1.25 | 1.23 |
| std | 0.27 | 0.00 | 0.24 | 0.00 | 0.04 | 0.00 | 0.21 | 0.00 | 0.05 | 0.00 | 0.22 |
| CON | 0.15 | 0.00 | 0.14 | 0.00 | 0.02 | 0.00 | 0.24 | 0.00 | 0.25 | 0.00 | 0.25 |
| std | 0.15 | 0.35 | 0.12 | 0.04 | 1.15 0.12 | 0.18 | 0.18 | 0.07 | 0.25 | 0.21 | 1.20 0.24 |
| R | 1.14 0.15 0.15 | 1.33 | 1.09 0.12 | 1.08 | 1.15 | 0.93 | 1.18 | 1.02 | 1.19 0.25 | 0.98 | 1.20 |
| ۵ | 0.001 | 0.012 1.33 0.35 0.00 | 0.003 | 0.003 | 0.01 | 0.005 | 0.002 | 0 | 0.001 | 0 | 0.005 |

| Description channel clustering; essential for clustering NaCh and neurofascin at axon initial segments and is required for physiological levels | of sodium chainter activity. Mercurial-insensitive water Brain, eye, lung, kidney, heart. Channel 1 (mMIWC1); allows muscle | water and small solutes to pass Ryanodine receptor type-3; Skeletal and smooth muscle, CNS intracellular Ca2 + channels intracellular Ca2 + channels | Ryanodine receptor type 1 (MYM) Skeletal muscle gene); intracellular calcium | channel MB-IRK2 (second class of inward Heart, kidney, and skeletal muscle rectifier potassium channels); ion | channel Note that the state of the state o | The and 120, this flow designated as Y6 in literature); (NPY-V6); neuropeptide Y is an important regulator of energy balance in mammals through its orexigenic, antithermogenic, and insulin secretagogue actions; expressed abundantly in the central nervous system; NPY receptors mediate a variety of physiological responses including physiological responses including feeding and vasoconstriction feeding and vasoconstriction glycogen subunit; phosphorylase kinase, gamma Heart, skeletal and cardiac muscle subunit; phosphorylase and fnot in liver and the liver gamma subunit activates the catabolism of CDNA) glycogen in skeletal muscle gamma subunit initiates the catabolism of CDNA) |
|---|---|--|---|---|---|---|
| GenBank | U48397 | ET61090 | X83932 | X80417 | :XVASCULAR:SMOQIH:MUSCUBLS在最后的 | J03293 |
| std | 0.25 | 0.37 | 0.23 | 0.24 | 0.10 | 0.71 |
| »s | 1.05 | 1.56 | 1.24 | 0.00 1.28 | 1.15 | 0.79 |
| std | 0.35 | 0.00 | 0.16 | 00.00 | 0.03 | 0.00 |
| Z O O | 0.34 | 0.00 | 0.43 | 0.00 | H.MUS 0.02 | 00.00 |
| std | 0.08 | 1.06 0.15 | 1.17 0.23 | 0.48 | 3MOQ1 0.15 | 0.24 |
| క | 1.37 | 1.06 | 1.17 | 1.25 | ULAR 1.00 | 04.1 |
| ۵ | 0.007 | 0.000 | 0.005 | 0.004 1.25 0.48 0.00 | WASC 0 | 0.021 1.40 0.24 |

| Location Location Thrombin receptor (PAR-1); Blood, platelets, monocytes; Transmembrane G-protein endothelial cells; cardiomyocytes; Transmembrane G-protein endothelial cells coupled receptor; activated by neuronal and glial cells serine protease cleavage; thrombin is a serine protease generated by the activation of the blood coagulation cascade following vessel injury; thrombin acts as a mitogen and apoptosis | inducer i 0.00 0.00 1.56 0.37 ET61090 Ryanodine receptor type-3; Skeletal and smooth muscle, CNS intracellular Ca2 + channels intracellular Ca2 + channels | Mouse cyclic GMP-dependent Brain, kidney, small intestine, colon protein kinase II; signal | transduction Mouse Kruppel-like gene (MKr2); Restricted to central and peripheral differentiation and/or phenotypic neurons of adults | maintenance of neurons Activin receptor-like kinase-6; Developing mosenchyme, muscle, receptors for morphogenic blood vessels, CNS, ear, eye, receptors for morphogenic blood seithelium | proteins; serine-threonine kiriase opinionali. Rck gene; protein kinase respiratory and choroid plexus respiratory and choroid plexus | Tbc1; domains homologous to Not well-characterized: te-2 oncogene and yeast mitosis hematopoietic cells, testis and regulators BUB2 and cdc16; kidney | nuclear localization LUN transcription factor; Lung bronchiolar epithelium and type forkhead domain identical to the II pneumocytes; tissue distribution HFHB gene; Cterminal region not well characterized | similar to the MFH8 gene Zinc finger protein 60 (ZFP60); Expressed transiently during in vitro Zinc finger protein 60 (ZFP60); Expressed transition Kruppel associated boxes muscle differentiation DNA-binding transcription factor CNS; tissue distribution not well (Emb); class VI POU domain characterized |
|---|---|--|---|--|---|---|--|---|
| GenBank U36757 | ET61090 | L12460 | Y00850 | 223143 | X66983 | 033005 | Y12293 | U48721 D13801 |
| std 0.28 | 0.37 | 0.15 | 0.12 | 0.35 | 0.12 | 0.54 | 0.11 | 0.15 |
| sw 1.32 | 1.56 | 1.10 | 1.48 | 1.04 | 1.12 | 1.18 | 1.08 | 1.04 |
| std 0.27 | 0.00 | 0.00 | 0.00 | 0.24 | 0.39 | 0.00 | 0.03 | 0.00 |
| 0.61 | 0.00 | 0.0 | 0.00 | 0.40 | 0.44 | 0.00 | 0.03 | 0.00 |
| std 0.26 | 0.15 | 0.51 | 0.15 | 0.08 | 0.38 | 1.06 | 0.18 | 0.20 |
| 1.12 | 1.06 | 0.77 | 0.96 0.15 | 1.13 0.08 | 1.26 0.38 | 1.79 1.06 | 0.98 | 1.18 |
| O.0044 | 0.000 1.06 0.15 | 0.013 0.77 0.51 | 0.000 | 0.022 | 0.044 | 0.048 | <0.001 0.98 0.1 | <0.001 1.18 0.20 0.003 1.43 0.41 |

| | of slls | > | | | | = | | | | | | | | | <u>.</u> | . e | | | | | | : |
|---|---|---|---|--|------------------------|--|--|------------------------|--|--|--|---------------------------------|-----------------------------------|-------------------|----------------------|---|------------------|--------------------|------------|----------------|--------------|-------------------|
| | ຮ | actor | | | | š | | | | | | | | | סטאינ | Nude gene (Whn) winged helix in adult thymus and shir, amoryomo transcription factor (amily; nails, nasal passages, tongue, palate | | | | | | |
| NS | ursor | d olf | | | | 5 | | tioe | | | | | | | E d | gue, | | | | | | |
| od C | rly precursors endocrine | iaan eelis | | | | ution | C G | intes | | | | | | | | , tor | | | | | | 7 |
| ежез | early endo | retin | | | | istrib | l sple | poe |) | ť | | | | | 7 | sages | | | | | | |
| o to | | esis, sells; e/bas | | | | و چ چ | s and | puel | | , hea | | | | | 9 | pas | | | | | | 1 |
| on priner | and | rogen glial (tellat | | | | tissi terizo | teste | 2 | <u>.</u> | brain | lasts | | 9 | <u> </u> | ٩ | nasal | eth | | | | | , |
| Location (Pax-6); Development of eye and CNS | (ngn3); CNS and neuroD- pancreatic | (embryogenesis) CNS, glial cells; retina ai bulb; stellate/basket cells | SNS | | rain | Brain; tissue characterized | Irain, | ž v | Intestinal tyrosine kinasa; protein warminary grand con- | MR-PTPmu; receptor-like protein Lung, brain, heart | Fibroblasts | | 444 | receptor; Unknown | 1 | n adu iails, | factor and teeth | | | | | |
| 9); D | 3); C | ă ă Ç | | (gi | subunit Brain | 85; | ntal B otor | dio. | | tein L | u_ | the | <u> </u> | ָרָסָרָי נסיי | - | elx z'y: | ctor a | ting | guit. | rols | one | |
| (Pax- | (ngr neur | recep | receptor CNS nding of | ric a | subi | epto | MDK1 (mouse developmental kinase 1); member of receptor | | <u>.</u> | bro | Ō. | peptide receptor; member of the | G protein-coupled receptor ramily | recep | - | fan | ğ | by differentiating | including | controls | immune | |
| | ÿ | ate | e Bir | obut, flux | ŏ | n rec | evelc | > | nase | r-like | e easin | ешре | cepto | | | wing tor | £ | differ | | also | the | |
| protein | 3 factor; | related bHLHprotein Metabotropic glutar 9: G-protein coupled | zepin | GABA (gamma-aminobut to inhibitory chloride flux | receptor | otoni | e mber | tyrosine kinase family | ž X | cepto | tyrosine phosphatase Bombesin/qastrin-releasing | ۲. E | 면. 명 | G-protein coupled | poorly characterized | /hn) wir factor | growth | <u>≻</u> | cells | ē | , | ius. |
| ×c | <u> </u> | L'Hpropic g | zodia bunit | y chi | 2 | a ser | ame : | nase | tyros | e. '. | nospr gastr | cept | coup | ខ | racte | ڪ ويو | | | • | tes; | | thyn |
| iptior D b | ranscription Veurogenin ranscription | related bHLHprotein Metabotropic glutan a: G-protein coupled | \-ben | \ (gar iibitor | Glutamate GluR5-2c. | E bet | - 0 | ine ki | Intestinal tyrosi pyrocine kinase | TPm. | ine pl Sesin/ | de re | tein- | tein. | y cha | Nude gene | modulates | production | eliat | keratinocytes; | development | system in thymus. |
| Description Paired box pro | rranscripuol Neurogenin transcriptiol | related bHLHprotein Metabotropic glutamate receptor CNS, glial cells; retina and olfactory 8. Gardein compled | GABA-benzodiazepine receptor heta-3 subunit: link binding of | GABA (gamma-aminobutyric acid) to inhibitory chloride flux | Glutamate GluR5-2c. | THIS beta serotonin receptor; G Brain; tissue distribution not well contein coupled receptor | most impuse developmental Brain, testes and spleen kinase 1); member of receptor | tyros | Intes | MR-F | tyros | pepti | ğ | g-pro | pood | Nude trans | mod | prod | epithelial | kerat | deve | svste |
| | | | 0. | | | | 32 | | 2,2 | 37 | Q | } | | 61 | | 56 | | | | | | |
| GenBank X63963 | U76208 | U17252 | U14420 | | X66118 | 214224 | X79082 | | 248757 | X58287 | M61000 | 2 | | ET61461 | | ET63226 | | | | | | |
| σ× |) | 5 |) | | × | N | * | | N | ^ | 2 | | | | | | | | | | | |
| std 0.09 | 0.19 | 0.32 | 0.17 | | 0.07 | 0.04 | 0.29 | | 0.27 | 0.37 | 14 | <u>-</u> | | 0.25 | | 0.20 | | | | | | |
| | 1.07 | 1.28 (| 1.06 | | 1.07 | 1.05 | 1.26 | | 1.30 | 1.19 | | | | 0.1 | | 96.0 | | | | | | |
| SW 1.06 | | | | | | | | - | | | | | | | | | | | | | | |
| std 0.00 | 0.00 | 0.12 | 90.0 | | 0.16 | 0.10 | 0.03 | | 0.01 | 0.00 | 6 | 5 | | 0.16 | | 0.18 | | | | | | |
| 0.00 0.00 | 9. | 0.07 | 0.04 | | 60.0 | 90.0 | 0.02 | | 10.0 | 0.00 | 8 | 3 | | 0.09 | | 0.50 | | | | | | |
| p 69 | 07 0 | 31 0 | 05 0 | | 0.22 | 33 | .29 | | .22 | .16 | , |) - | | 18 | : | 1.14 0.10 0.50 | | | | | | |
| CR std 1.07 0.69 | 0. | 1.15 0.31 | 2 0. | | - 0 | 1 0 | 0 | | 0 | 0 | | 0 | | 1.20 0.18 | · | 4 0 | | | | | | |
| 2.5 | 1.0 | | 0.0 | | - | | 1.2 | | 1.2 | 7 | | <u>-</u> | | | | | | | | | | |
| P 0.026 | <0.001 1.07 0.02 0.00 | 0.003 | <0.001 1.02 0.02 0.04 | | <0.001 1.11 | 0.001 1.11 0.33 | 0.001 1.21 0.29 | | <0.001 1.20 0.22 0.01 | 0.001 1.11 0.16 | | <0.001 1.11 0.17 0.00 | | 000 | 3 | 0.009 | | | | | | |
| Ö | V | Ó | V | | V | 0 | 0 | | V | c | , | v | | C | , | 0 | | | | | | |

system in thymus <u>据文献经验介绍。《文文》(文文文)(111)(120)的TREPORTEDIN WOVERSHORMONE CERONATH FACTOR IN ACTOR IN A</u>

-74-

| | | | 17 | | | | | | | | | | | | | | | | |
|----------------------|--|---|--|--|---|--|----------------------------------|---|----------------|---|---|---------------------------|--|---|----------------------|--|--|--|--------------------------------|
| | anterior | anterior | Translation of | nesoderm 1 limb | | | | sodermal | embryo, | mesoderin, | vibrissae, kidney | | in £13.5 ication of | | e tubular ney and | cells in | | ogenesis; : liver | |
| | the | the | | e gud | | | | nbryo | ō | _ | thes, n and | | ear pecif | | es ar kid | thelia | | adult | |
| | ō | ō | | ogenesis heart | | | | genesis; nouse en | Ticcips | paraxial | chial arc s systen | enesis | NS and | | ajor site Ils in | euroepit | | mouse (| |
| Description Location | beta) Follicle stimulating hormone beta Gonadotropes subunit (FSH-beta, gonadotropin); pituitary | stimulates development of follicle and spermatogenesis | 0.004 0.91 0.33 0.21 0.34 1.49 0.09 0.23 できます regulation of reproduction pituitary regulation of reproduction pituitary regulation of reproduction pituitary case of the production pituitary case of the pituitary case o | T gene (Brachyury genel); T-box Early embry family; sequence specific DNA-formation; | binding protein that functions as morphrogeness: a transcription activator; required | for morphogenesis of mesoderm- derived structures, control of | gastrulation; development of the | Mox-1; homeobox gene; marker Early embryogenesis; mesodermal epithelial-mesenchymal patterning in mouse embryos | transformation | Fkh-2; a forknead/winged lieux ivollidiod transcription factor | somites, branchial arches, vibrissae, central nervous system and kidney | rin F; Involved in axonal | guidance NK-related homeobox gene (Nkx- Developing CNS and ear in E13.5 NK-related homeobox gene (Nkx- Developing CNS and ear in E13.5 | 5.2); cell type specification of circles, one colls | il surfa | role in regulating cell cycle proliferating neuroepithelial cells in | progression during the transition brain, neurous of neural cells from proliferation | to differentiation. Retinoic acid-responsive protein Mid-gestation mouse embryogenesis; | (MK); growin dingrammer factor |
| GenBank | U12932 | 36126 | FMBRYONIC | X51683 | | | | 215103 | | X86368 | | X97817 | 880989 | | X83577 | | | M34094 | |
| std | 0.12 | o o | O.OS | 0.33 | | | | 0.37 | | 0.21 | | 0.19 | 0.21 | | 0.13 | | | 0.21 | |
| ΝS | 1.11 | | i.40 Joreni | 0.98 | | | | 1.17 | | 0.91 | | 1.09 | 1.10 | | 1.22 | | | 1.08 | |
| std | | | 0.34 | 0.00 | | | | 0.00 | | 0.18 | | 0.00 | 0.46 | | 0.24 | | | 0.10 1.08 | مر |
| NO O | 0.39 | | 0.21 | 0.00 | | | | 0.00 | | 0.22 | | 0.00 | 0.40 | | 0.50 | | | 0.11 | |
| std | | | 0.33 | 0.09 | | | | 0.10 | | 0.08 | | 0.02 | 0.50 | | 0.21 | | | 0.03 | |
| ä | | | 0.91 0.33 0.21 | 1.06 0.09 0.00 | | | | 1.09 0.10 | | 1,08 0.08 | | 1.10 | 1.78 0.50 0.40 | | 1.00 0.21 0.50 | | | 1.03 | |
| ۵ | 7 | | 0.004 | 0.001 | | | | 0.001 | | 0.001 | | Z 0.001 1.10 0.02 | 0.018 | | 0.011 | | | 0 | 1 |

| | Hox 3.3; homeobox transcription Spleen, bone marrow factor; embryogenesis; | expressed vibrissae, lungs, body wall, stomach, formation gonads, ribs, limbs, shoulders ach digit olfactory region, eye, stooth primordium, esophagus, mesonephros, dorsal root ganglia and is strongly expressed in the spinal | cord. Atrial natriuretic peptide Epithelial and endothelial cells; lung clearance receptor (ANP-CR or (smooth muscle cells), heart (aortic NPRC); membrane protein; smooth muscle cells), placenta modulates availability of | | | | |
|--|--|--|---|---|---|--|---|
| Location Embryo | pleen, | Embryo: vibrissae, lu gonads, ri olfactory primordium, mesonephro is strongly | cord. Epithelia (smooth smooth | | estis | and Kidney rter; | SNS |
| L actor E | ption S lesis; | limb E sssed v ation g ation g igit o | c sptide E R or (s otein; s | rarger protein- system; may southelial odulates ctivated igulation | ein 1 T | 0 | and CNS nalian |
| tion f nent | ox transcription embryogenesis; | eptor; expre e form | iuretic peptide sptor (ANP-CR or mbrane protein; availability of | uretic peptides at target ms; activation of G protein-lided signaling system; withdist permability; may ulate angiogenesis by sition of vascular endothelial growth factor; modulates vity of mitogen-activated sin kinase (MAPK, regulation) | 的情况是因为是一种的一种的一种的一种的一种的一种的一种的一种的一种的一种的一种的一种的一种的一 | sodium and cotransporter; | orotein formation and of mammalian |
| anscrip evelopr | eobox eml | s IB rec vith th lanx of | natriuretic receptor (A membrane availabi | peptides at vation of G p signaling s permability; angiogenesis vascular endo f factor; moof mitogen-ac se (MAPK, regeration) | complete of cl | | e prote form of |
| tion sox tr limb d | 3; hom | opoiesi: type ment; ently v | nati se rec me | tic pe activa activa lial signalial te control of vowth of control of vorth | onemal pairin | nelosis 9-sensii | ambran orevin; sance |
| Locatior Homeobox transcription factor Embryo (EVX2); limb development | Hox 3.5 | haematopoiesis Activin type IB receptor; limb Embryo: development; expressed vibrissae, coincidently with the formation gonads, of the last phalanx of each digit olfactory mesonep | Atrial clearance (NPRC); | natriuretic peptides at target organs; activation of G protein-coupled signaling system; endothelial permability; may modulate angiogenesis by inhibition of vascular endothelial cell growth factor; modulates activity of mitogen-activated protein kinase (MAPK, regulation of cell proliferation) | Indianal Complex | during melosis Thiazide-sensitive chloride | transmembrane protein Dystrobrevin; format maintenance of n |
| GenBank M93128 | X16510 | 231663 | D78175 | | KNOTIREPORTED/INTAVERSOMBIREPORTERS/ILGERINGERS/ILGERINGERSOMBIRES/ILGERINGERS/ILGERS/ILGERINGERS/ILG | U61085 | X95226 |
| std 0.15 | 0.10 | 0.18 | 0.13 | | 0.22 | 0.19 | 0.44 |
| 3w 1.03 | 1.16 | 1.18 | 1.10 | | 1.05 | 1.21 | 1.46 |
| std 0.00 | 0.12 | - 000 | 0.20 | | <u>) 1167.世界</u> 0.21 | 0.19 | 0.30 |
| 0.00 0.00 | 0.13 | 0.00 | 0.12 | | 0.18 | 0.11 | 0.34 |
| std 0.09 | 0.15 0.13 | 1.09 0.16 | 90.0 | | 0.07 | 0.86 0.29 | 0.36 |
| R 1.1 | 1.04 | 1.09 | 0.99 | | 1.43 | 0.86 | 1.20 |
| ٥٥ | 0 | 0 | 0 | | KNOTIREPORTED INIT 0.000 1.43 0.07 | 0.003 | 0.024 1.20 0.36 0.34 |

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| Description Location neuromuscular junction | Membrane metalloendopeptidase Kidney, bone homologue (Pex); mineralization of extracellular matrix by | osteoclasts Kappa-casein; milk protein Mammary glands Repetin; similar to intermediate Epithelia of forestomach and tongue filament-associated proteins profilaggrin and trichohyalin; expression during late epidermal | differentiation Fibroblast growth factor CNS homologous factor 4 (FHF-4); involved in nervous system | Zinc finger proteins (mkr3,4,5) Whole embryo, testes in adult Zinc finger proteins (mkr3,4,5) Whole embryo, testes in adult N-glycan alpha 2,8- Lung, heart, spleen, brain sialyltransferase (STSia IV) | Rod transducin alpha subunit (1r- Hetina, not reputed in 1705, 2007), alpha); couples photolysis of heart rhodopsin to activation of cGMP phosphodiesterase; visual signal | sils | erine Salivary glands; crosshybridization with kallikreins | exch: | Hyaluronan synthase 3; Eyes, Kluirey, Cilorial Co. You polymerizes hyaluron, (extracellular) glycosarninoglycan; can be hallmark of tissue remodeling; reduces cell motility; | -92- |
|--|---|---|--|---|--|--------|--|-----------|---|------|
| GenBank | U73915 | M10114 X99251 | U66204 | M36516 X86000 | M25513 | X12875 | Y00500 | X63100 | ET62673 | |
| std | 0.10 | 0.13 | 0.29 | 0.10 | 0.33 | 0.25 | 0.30 | 0.25 | 0.28 | |
| 8W | 96.0 | 1.13 0.90 | 0.98 | 1.10 | 1.12 | 1.82 | 1.12 | 0.85 | 1.06 | |
| std | 0.00 | 0.38 | 0.22 | 0.27 | 0.36 | 0.40 | 0.38 | 0.45 | 0.45 | |
| CON | 0.00 | 0.35 | 0.30 | 0.36 | 0.40 | 0.23 | 1.44 0.41 0.49 | 0.29 | 0.41 | |
| std | 0.32 | 0.10 | 1.26 0.18 | 0.10 | 0.11 | 0.51 | 0.41 | 1,18 0.07 | 0.18 | |
| S | 1.38 | 1.10 | 1.26 | 1.06 0.96 | 1.21 | 1.18 | 1.44 | | 1.30 | |
| ۵ | 0.000 | 0.011 | 0.006 | 0.004 | 0.025 | 0.008 | 0.049 | 0.030 | 0.036 | |

| Description Location expecially in | soft connective tissue Actin capping protein; germ cell Haploid germ cells of testis gene 3 (gsg3); homologue of | Sufficient of the Carlotter of the Carlo | gous to elf-4A gene for sperm calmodulin | protein Meiosis-specific XMR; Testis; lymphoid cell lineages: nuclei transcriptional activator function? of spermatocytes, early in the prophase of the first meiotic division, and later becomes concentrated in the XY nuclear subregion | Testicular alpha tubulin Testis Ott, mouse X-linked multigene Expressed during meiosis family | Osteoblast specific factor 2 Osteoblastic cells (OSF-2); extracellular matrix? | Neuroendocrine protein 782; Widely distributed neuroendocrine secretory protein present in protein; neurons, endocrine cells; serum; proteolytic conversion and pituitary, cells producing insulin and activation of proprotein glucagon; melanosomes convertases 2 in the endoplasmic | reticulum Alpha1(XI) collagen (COL11a1); Embryo cartilaginous tissue, brain, structural integrity; essential for heart, tongue, intestine, and otic normal cartilage development vesicles | Seminal vesicle secretory protein Seminal vesicles IV (SVS IV); major secretory protein of seminal vesicles; regulation of the immune response, blood coagulation; | -77- |
|------------------------------------|--|--|--|--|---|--|--|--|--|------|
| GenBank (| D87471 | J04847 | 246299 | X72697 | M19413 X96606 | D13664 | X15830 | D38162 | M35732 | |
| std | 0.11 | 0.29 | 0.29 | 0.09 | 0.26 | 0.10 | 0.39 | 0.67 | 0.04 | |
| SW | 1.12 | 1.26 | 1.19 | 1.08 | 1.07 | 1.23 | 1.40 | 1.27 | 1.56 | |
| std | 0.00 | 0:30 | 0.02 | 0.23 | 0.02 | 0.22 | 0.15 | 0.59 | 0.37 | |
| CON | 0.00 | 0.48 | 0.01 | 0.14 | 0.02 | 0.13 | 0.09 | 0.53 | 0.43 | |
| std | 0.92 | 1.16 0.14 | 0.14 | 0.05 | 0.18 | 0.31 | 0.43 | 1.10 0.80 | 0.03 | |
| S | 1.81 | 1.16 | 1.09 | 1.05 | 1.20 | 1.14 | 1.33 | 1.10 | 1.0 | |
| ۵ | 0.017 | 0.019 | <0.001 1.09 0.14 0.01 | <0.001 1.05 0.05 | <0.001 <0.001 | 0.002 | 0.006 | 0.440 | 0.002 | |

| | = | | ₽ ≿ | | | . c · | |
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| | adu. | | in ar enso | | | | |
| | ent in | | cells hanos dult | | | repor | |
| | t pres | St. | d by mecl | | | not | |
| | ou pa | ë E | oresse the obryo | istets istets um. iis | Φ | stine, | |
| | eport | nantly | r: ext Sing in en | s and s and sitheli | en lin | inte | |
| Location | estis (r ver) | redomi | Inner ear; expressed by cells in and surrounding the mechanosensury epithelia in embryo and adult | Pancreas and islets Pancreas and islets Nasal epithelium. Spermiogenesis | Male ge | (idney, iver | Festis |
| ٦ - ا | inflammatory reproduction Y chromosome RNA transcript Testis (reported not present in adult expressed in testis (pY353/8); liver) | protein product uncharacterized; sex determination factor? Intracellular serine proteinase Predominantly in testis inhibitor (mBM2A); serine proteinase inhibitors (serpins) are | regulators of extracellular protectives protectives of ear; expressed by cells in and Beta-Tectorin; extracellular matrix inner ear; expressed by cells in and surrounding the mechanosensury protein embryo and adult | bunit; a | protein; a component of the cytoskeletal calyx of the mammalian sperm head. T-complex responder (Tcp-10); Male germ line fcp-10 gene has been established as a molecular for the T complex | responder locus which plays a central role in the transmission ratio distortion phenotype expressed by males heterozygous for a Thaplotype. Meprin beta subunit isoform Kidney, intestine, not reported (Mep-1beta); meprins are liver membrane bound oligomeric | |
| | RNA estis (| uct unchar ation facto serine (mBM2A): hibitors (se | of e) extracell | ne II ne I protein beta 3 of ac | mponent calyx o rm head. ponder (a has s a rr the T | the transfion phe ion phe ales hetero le. subunit i meprins identification of the contraction of the contrac | ta subu |
| c | ory on usome in t | roduct ninatio ar se mE (mE | s orin; e | Jin ge Jin ge inding protein form | tal call and sperm of as for the | role in the distortion of by males haplotype. beta suburets) mee | dope /or be rial pro |
| Description | inflammatory reproduction Y chromosome expressed in te | protein product uncharae sex determination factor? Intracellular serine pri inhibitor (mBM2A); proteinase inhibitors (serf | regulators proteolysis Beta-Tecto protein | Preproinsulin gene II Preproinsulin gene I Odorant binding protein Ib Capping protein beta 3 su novel isoform of actin | protein; a component cytoskeletal calyx cytoskeletal calyx cytoskeletal calyx cytoskeletal sperm head. Tcp-10 gene has established as a mandidata for the T | responder locus central role in the ratio distortion expressed by male for a T haplotype. Meprin beta st. (Mep-1beta): membrane-bound | metalloendopepingses. alpha and/or beta subunit Perforatorial protein (PER |
| GenBank | X05260 | 1086701 | ET63122 | X04724 X04725 ET63205 ET63408 | X58169 | ET61364 | ET62832 |
| std | . 96.0 | 1.74 | 0.20 | 0.21 0.46 0.32 0.21 | 0.81 | 0.25 | 0 47 |
| SW | 0.97 | 1.46 | 1.1 | 1.15 1.63 1.20 1.51 | 0.93 | 1.72 | 1 37 |
| std | 0.00 | - 00 | 0.08 | 0.31 0.00 0.00 | 0.0 | 0.00 | 6 |
| CON | 0.00 | 0.00 | 0.58 | 0.25 0.06 0.00 0.00 | 0.00 | 0.00 | , |
| std | 0.72 | 0.65 | 0.39 | 0.05 0.39 0.44 0.33 | . 0.21 | 0.81 | 9 |
| 8 | | 2.86 | 1.42 0.39 | 1.00 1.21 1.51 1.18 | 1.24 | 1.45 | , |
| ۵ | 0.043 1.87 | 0.046 | 0.019 | 0.005 0.004 0.002 0 | 0.045 1.24 0.21 0.00 | 0.011 1.45 0.81 | |

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| tion testicular price se similarities to a | major sperm | Odorant receptor 23 (OR23) Ultactory and destroued certs A-myb; a conserved member of Abundant expression in testis (germ) the Myb proto-oncogene family, cell differentiation); low level encodes a sequence-specific expression in ovary, spleen (B DNA binding protein (A-Myb) that lymphocytes) and brain; CNS in binds to and transactivates embryos | promoters containing myb-binding sites binding sites Pax-4; a paired-box transcription Pancreatic islet endocrine progenitor factor that plays an important cells role in the development of | pancicatic dutations of the period of the protein 70-2 Male germ cells (HSPO.2); not induced by heat shock; developmentally regulated in commandation cells; critical | role in spermatogenesis G protein alpha olfactory subunit; Olfactory epithelium sensory transduction | Involucrin; a glycine, serine- and Epidermis cysteine-rich protein expressed late in differentiation of grandular | layers in normal epidermis DNA ligase III-beta; DNA ligase III Alpha is expressed in most tissues: exists as two distinct isoforms beta is expressed in testes and denoted alpha and beta during sperinatogenesis | 25-hydroxyvitamin D3 24- Kidney and intestine. hydroxylase; metabolism and reoulation of vitamin D3 | Beta-casein gene Mammary glands -79- |
|---|----------------|--|--|---|--|---|---|---|---|
| GenBank | | ET62968 ET63528 | ET63177 | M20567 | ET61399 | L28819 | ET62336 | D49438 | M26940 |
| std | | 0.40 | 0.39 | 0.33 | 0.38 | 0.57 | 0.26 | 0.11 | 0.59 |
| »s | ٠. | 1.17 | 1.14 | 1.37 | 0.00 1.10 | 1.16 | 1.17 | 1.13 | 1.22 |
| std | | 0.26 | 0.00 | 0.07 | 0.00 | 0.15 | 0.09 | 0.12 | 0.00 |
| N 00 00 | | 0.24 | 0.00 | 0.04 | 1.30 0.05 0.00 | 0.09 | 0.05 | 0.07 | 1.27 0.28 0.00 |
| std | | 0.33 | 0.46 | 1.06 0.22 | 0.05 | 1.07 0.08 | 0.52 | 0.18 | 0.28 |
| CA | | 0.94 | 1.44 | 1.06 | 1.30 | 1.07 | 1.45 | 0.95 | 1.27 |
| م ـ | | 0.016 | 0.005 1.44 0.46 0.00 | 0.001 | 0.001 | 0.015 | 0.005 | 0 | 0.011 |

| Description Mammary glands Lysozyme; signaling molecule for Macrophages, paneth cells (located mast cells which respond with in duodenal crypts) | histamine secretion teneral programment of the prog | Amphiphysin II; endocytosis and Macrophages, neurons, germ cens, signal transduction (recycling endocrine tissues | synaptic vesicle components) T1-cadherin, calcium-binding Thymocytes | cell adhesion molecule (CAMs). Integrin alpha-4; cell adhesion | Erythrocyte band / Integral Spreen, Iding, (Cons.), Inc. Communication of the membrane protein; protein 7.2b; liver | stomatin | CTLA-2-beta; nomologue to rema | Cell and processing CD53; Thymocytes | membrane glycoprotein | Gp91phox (Cybb); phagocyte Phagocyte cytochrome b558; heterodimer | comprised of gp91phox and | p22phox; a flavocytochrome that | mediates the transfer of electrons | in the respiratory burst Oxidase | Potassium channel gene (MK2); T cells; myelinating Schwann cells | shaker subfamily | Homologue of the rat T cell Cytotoxic Liymphocytes differentiation marker RT6; cell- | cell signaling | MCSP-1 CTL serine protease 1; I lymphocytes may play a role in cytolytic | C | Interleukin-1 bata converting Monocytes and macrophages | -80- |
|--|---|---|---|--|---|----------|--------------------------------|--------------------------------------|-----------------------|--|---------------------------|---------------------------------|------------------------------------|----------------------------------|--|------------------|--|----------------|---|---|---|------|
| GenBank V00740 V00428 | | U86405 | U69136 | X53176 | X91043 | | X15592 | X97227 | | 043384 | | | | | M30440 | | X52991 | | X14092 | | 004269 | |
| o.10 0.07 | | 0.16 | 0.44 | | 0.24 | | 0.15 | 0.20 | | 0.19 | | | | | 0.39 | | 0.35 | | 0.11 | | 0.30 | |
| SW 1.12 1.07 | | 1.09 | 0.94 | 1.32 | 1.14 | | 1.12 | 1.12 | | 1.27 | | | | | 1 16 | : | 1.35 | | 0.97 | | 1.07 | |
| std 0.05 0.04 | | 0.42 | 0.19 | 0.20 | 0.05 | | 0.12 | 0.26 | | 0.05 | | | | | 0.26 | 9.5 | 0.00 | | 0.00 | | 0.50 | |
| CON 0.05 0.02 | | 0.45 | 0.11 | 0.16 | 0.03 | | 0.14 | 0.15 | | 0.03 | | | | | 7 | | 0.00 | | 0.00 | | 0.29 | |
| std 0.29 0.08 | | 0.26 | 1.02 0.02 | | 0.15 | | 0.06 | 1.11 0.15 | | 0.20 | | | | | | 2.0 | 0.29 | | 0.11 | | 0.33 | |
| CR 1.03 | NOT | 1.24 0.26 0.45 | 1.02 | 131 | 1.27 | | 1.06 | 1.1 | | 1.10 | | | | | | 1.20 | 0.99 | | 1.37 | | 1.36 | |
| 9.00 1.00 | "IBLOOD NOT SHIP | 0.037 1.24 | 0.013 | 900 | < 0.001 | | <0.001 1.06 0.06 | 0.002 | | <0.001 1.10 | | | | | 0 | 0.002 | 0.002 | | 0.000 | | 0.033 | |

| Description enzyme (ICE); may mediate endotoxin-induced cholestatic effect of decreased hepatocellular bile salt uptake; IL-1DOWN in CR Differentiation antigen (CD22); B cells | negratus o cei interescente de la condition de | receptor Class I recognizing receptors Subpopulation of natural killer cell involved in ability of F1 hybrid mice to reject parental H-2d bone | marrow cell grafts Terminal deoxynucleotidyltransferase; template-independent polymerase; VDJ assembly; | recombination Lymphocyte specific helicase; T and B cells at both the immature putative role in replication, repair, and mature stage; not in heart, liver, recombination and transcription lung, muscle, brain or kidney | P500/TCA3; SIS-epsilon; small, T cells, myeloid and lymphoid cells secreted, and inducible protein; expressed more abundantly in activated mouse helper T cells | than by resting T cells Mast cell protease 7 (mMCP-7); Mast cells mouse mast cell tryptase 2; released when mast cells are | ACIVATION Mast cell protease-4 tissue tissue MAST GENERAL SOUGTION FRECEPTOR CONTROLLINE MAST NET SIGNAL TRANSPUCTION FRECEPTOR CONTROLLINE MAST NET SIGNAL TRANSPORT FRECEPTOR CONTROLLI | 文章 1.06 0.10 0.30 0.53 1.15 0.21 X51468 Preprosomatostatin; precurser Macrophages; nervous system 0.038 1.06 0.10 0.30 0.53 1.15 0.21 X51468 Preprosomatostatin; precurser Macrophages; nervous system peptide cleaved to release |
|---|--|---|---|--|---|--|--|---|
| GenBank L16928 | ET62844 | U49866 | X04123 | U25691 | M23501 | ET61471 | M55617 | X51468 |
| std . 0.06 | 0.44 | 0.18 | 0.17 | 0.54 | 0.62 | 0.23 | 0.33 | 0.21 |
| sw , 1.07 | 0.94 | 0.98 | 1.05 | 1.51 | 1.93 | 0.34 1.11 | 1.41 | 1.15 |
| std 0.41 | 0.34 | 0.50 | 0.21 | 0.00 | 0.00 | 0.34 | 0.00 | 0.53 |
| CON 0.24 | 0.24 | 0.31 | 0.38 | 0.00 | 0.00 | 0.20 | 0.00 | 0.30 |
| std 0.47 | 0.13 | 0.39 | 1.07 0.07 | 0.51 | 0.45 | 0.13 | 0.31 | 。 0.0 |
| CR 1.47 | 1.20 | 1.3 | 1.07 | 1.53 | 1.07 0.4 | 1.08 | 1.10 | 1.06 |
| P CR std CON | 0.027 1.20 0.1 | 0.046 1.31 0.3 | 0.003 | 0.007 | 0.005 | 0.007 1.08 0.1 | 0.001 1.10 0.31 0.00 | 0.038 |

-81-

| Description somatostatin which regulates T cell IFN-gamma production Interleur, 2 (1L-2); stimulates Helper T cells | promotes and hypphocytics and helper T cells and interleukin-6; promotes B cell Some helper T cells and maturation to lg- secreting cells; macrophages helps activate T cells | Interleukin 7 (IL-7); growth factor B cell progenitors Macrophage inflammatory MIP-1alpha RL2 in liver and spleen protein-1 alpha receptor; mediates growth inhibitory | effects of the chemokine Macrophage inflammatory Macrophages protein-2 (MIP2); small inducible cytokine subfamily member | Macrophage inflammatory protein Thymus, heart, spleen, and livef; to receptor 1-alpha 2; Induces lesser extent in the lung and brain mobilization of intercellular | calcium; leucocyte chemoattractant Interferon beta (type 1); growth Uniquitous factor; T helper cell differentiation factor; antiviral; modulates immune responses to foreign and self-antigens | Interferon beta (type 2) Interleukin 2 receptor; cytokine T cells receptor receptor | Complement receptor type 2.22.5. Personal (CR2) (CR2) Protein-serine/threonine kinase Blood, epithelial and CNS embryonic (pim-2); cell proliferation; highly development expressed in mitogenically (cytokines) stimulated hematopoiotic cells; evokes longherm potentiation in hippocampus |
|---|---|--|--|--|---|--|--|
| GenBank M16762 | X54542 | X07962 U28404 | X53798 | ET62976 | V00755 | V00756 M26271 | M35684 L41495 |
| std 0.69 | 0.34 | 0.24 | 0.17 | 0.22 | 0.13 | | 0.10 |
| SW 1.03 | 1.30 | 1.40 | 1.00 | 1.25 | 1.04 | 1.10 | 2.15 |
| std 0.30 | . 0.18 | 0.38 | 0.21 | 0.13 | 0.35 | 0.00 | 0.09 |
| CON 0.17 | 0.54 | 0.22 | 0.12 | 0.07 | 0,44 | 0.00 | 0.05 |
| std 0.46 | 0.06 0.54 | 0.08 | 0.28 | 0.11 | 0.23 | 0.19 | 0.65 |
| CR 1.53 | 1.06 | 1.00 | 1.38 | 0.99 | 1.3 | 1.21 | 1.22 |
| 9 0.044 | 0.014 | 0.004 | 0.001 | < 0.001 | 0.015 | <0.001 | 0.010 |

-82-

| Description Cytosolic tyrosine protein kinase Lymphopoiesis; haematopoietic cells, Cytosolic tyrosine protein platelets, macrophages and SYK; signal transduction neutrophils | Calmodulin-dependent protein T cells kinase IV; multifunctional, serine- | threonine protein kinase Wee1 kinase; inhibits entry into Lymphocytes mitosis by phosphorylation of the | Cdc2 kinase Thrombin receptor (PAR-1); Blood, platelets, monocytes; transmembrane G-protein coupled endothelial cells; cardiomyocytes; receptor: activated by serine neuronal and glial cells | protease cleavage; thrombin is a serine protease generated by the activation of the blood | coagulation cascade following vessel injury: thrombin acts as a | mitogen and apoptosis inducet. T cell transcription factor NFAT1 T cells | isoform B Son of sevenless 2; Ras-specific T cells | exchange factors Son of sevenless 1; Ras-specific T cells | exchange factors Homeobox gene 2.6 (Hox-2.6) Whole embryo; in adult: blood cells, | transcription factor; embryonic stem cells and low levels in commissional development; haematopolesis and spermatogenic cells Ly-49F-GE antigen; NK cell NK cells | suface molecule; determinant of IL-2-activated NK cell specificity; inhibitory receptor for interaction | with MHC class I Antigen, B cell receptor | Mast cell protease 7 (mMCP-1), Mast cells mast cell tryptase 2; released | when mast cells are activated Protein-tyrosine phosphatase Hematopoictic tissues | -83- |
|---|--|---|---|---|--|---|---|--|--|---|---|---|---|---|------|
| GenBank ET61263 | X58995 | D30743 | U36757 | | | U36575 | 211664 | 211574 | M36654 | U10092 | | L43567 | ET61471 | ET61424 | |
| std 0.55 | 0.10 | 0.13 | 0.28 | | | 0.17 | 0.15 | 0.25 | 0.39 | 0 24 | • | 0.24 | 0.23 | 0.26 | |
| sw 1.17 | 121 | 1.14 | 1.32 | | | 1.05 | 1.13 | 1 22 | 1.43 | 1 22 | ! | 1.17 | 1.1 | 0.96 | |
| std 0.00 | 0.03 | 0.00 | 0.27 | | | 0.00 | 000 | 22.0 | 0.34 | | 3 | 010 | 0.34 | 0.00 | |
| 00.00 | 0.02 | 0.00 | 0.61 | | | 0.00 | | | 5 6 | | 9 | 76.0 | 0.20 | 114 0.05 0.00 | |
| std 0.36 | 0.11 | 0.42 | 0.26 | | | 0.13 | 9 | | 2 6 | | 1.30 0.84 | , | 1.08 0.13 | 0.05 | ; |
| CR 2.00 | | 1.22 | 1.12 | | | | | | - 6 | 70.0 | 1.30 | | | 1 14 | - |
| P 0.002 | <0.001 1.07 | 0.002 | 0.044 | | | 7 150 00 15 | | 00:00 | 0.002 | 0.020 | 0.034 | 6 | 0.003 | c |) |

| Description Sox4; transcription factor in the Thymus, bone marrow, and gonads Sox gene family with separable DNA-binding and transactivation domains | | PTX3, entraxins; include C.L.var, skeletal muscle and near, reactive protein (CRP) and serum amyloid P. component (SAP) | which are prototypic acute phase reactants that serve as indicators of inflammatory reactions. Interferon-activatable gene (204); Nucleoi mediates antimicrobial, immunomodulary and cell growth-regulatory activities of | Interferons, increased by North Control of the Cont | ST2L, primary response gene, i cens specifically induced by growth stimulation, highly similar to IL1 | receptor type 1 Fos-related antigen-1 (Fra-1) Spleen Immunity associated protein 38; Spleen inducible by malaria | TAL2 Zinc finger protein A20; activated Lymphocytes by T cell acute lymphoblastic | binding protein 4-18B ligand, inflamatory T cells response; member of the TNF | -85- |
|--|---|---|---|--|---|---|---|---|------|
| GenBank ET62444 | L24118 | X83601 | M31419 | THE PARTY OF | D13695 | U34245 Y08026 | M81077 U19463 | L15435 | |
| std 0.25 | 0.14 | 0.33 | 0.39 | HERFEIS | 0.17 | 0.39 | 0.20 | 1.23 | |
| SW 1.04 | 1.15 | 1.27 | 1.39 | E0: 18: | 1.00 | 1.40 | 1.23 | 1.40 | |
| std 0.14 | <u>SE GENES **LIVER: ** </u> | 0.00 | 0.00 | FGEN | 0.15 | 0.00 | 0.00 | 0.00 | |
| 0.21 | E GENE 0.22 | 0.00 | 00.00 | ESBONS | 0.09 | 0.00 | 0.00 | 0.00 | |
| std 0.03 | PONS 0.20 | 0.32 | 0.31 | ARWER | 0.17 | 0.46 | 0.36 | 0.24 | |
| 1.03 | RY RESPONS 0.91 0.20 | 1.19 | 1.09 0.31 | Wind | 1:1 | 1.28 | 1.35 | 1.27 0.24 | |
| g.00. | ESPRIMARY RESPON | 0.002 1.19 0.32 | 0.002 | | < 0.001 | 0.005 1.28 0.46 <0.001 1.04 0.04 | 0.001 1.35 (| 0.1 | |

| Description family; important for the generation of antiviral CD8 T cell | Elbroblasts and human monocytes Glucocortoid-regulated Fibroblasts and human monocytes inflammatory cyclooxygenase; prostaglandin G/H synthase, putative mediator of inflammation; mRNA and protein rise dramatically in response to growth factors, cytokines, and oncogene activation; suppressed by glucocorticoid hormone | Immune-responsive gene 1 (Irg1); Macrophages activated by bacterial LPS treatment | Gene induced by PDGF with Unknown | Some nomotory (1995年) | Cincination Structure of the Control of the limbs and thymic delation leads to partial syndactyly of the limbs and thymic delation leads to partial syndactyly of the limbs and thymic hyperplasia, suggesting impaired programmed cell death hyperplasia, suggesting impaired programmed cell death | ###################################### | Histone H1; chromatin structure Ubiquitous Histone H1b; chromatin structure Ubiquitous Histone H2B; chromatin structure Liver (ubiquitous) Histone H3.2-616, and histone Liver (ubiquitous) H2b-616; chromatin structure Histone H3.1-D (H3-D) and Ubiquitous histone H4-D (H4-D) genes; chromatin structure |
|--|---|---|-----------------------------------|--|--|---|--|
| GenBank | M88242 | L38281 | K02785 | CANNTRINGELLUIARITURNONER EFFORMER CONTRACTOR CONTRACTO | X71978 | (104141 L04141 | J03482 ET62262 ET62908 U62675 U62672 |
| std | 0.16 | 0.09 | 0.28 | 0.11 | 0.10 | 0.49 | 0.24 0.27 0.24 0.70 |
| »S | 1.03 | 1.16 | 1.31 | 1.37 | 0.00 1.02 0.10 | 1.79 | 1.08 1.09 1.10 0.79 1.12 |
| std | 00.0 | 0.00 | 0.03 | O.27 | 0.00 | 0.00 | 0.00 0.03 0.053 0.00 0.18 |
| CON | 0.18 0.00 | 0.00 | 0.02 | D.43 | 1.11 0.11 0.00 | O.00 | 0.00 0.03 0.00 0.00 |
| std | 0.18 | 0.12 | 1.15 0.32 | O.10 | 0.11 | 0.95 | 0.30 0.18 0.26 0.27 |
| ឌ | 1.18 | 1.07 | 1.15 | 0.95 0.95 | 1.1 | 1.33 | 1.74 1.69 1.41 1.20 1.08 |
| ο. | <0.001 1.18 | <0.001 1.07 | 0.001 | CENTRA 0.002 | 0 | VCHHOMATINASTRUCTURE 0.028 1.33 0.95 0.00 | 0.000 0.000 0.030 0.038 |

-98-

-87-

| Description Histone H2A; chromatin Ubiquitous | structure Histone H3.2-F (H3-F), histone Ubiquitous H2a.1-F (H2a-F), histone H2b-F H2b.1-Fi shromarin structure | nze-ri; chromann swoczer Htf9-c; structrural similarity with Liver (ubiquitous) yeast and bacterial nucleic acid- | modifying enzymes; activated at the G1/S transition, maximum and S phase; down in growth arrested cells | Homologous to Drosophila HP1 Ubiquitous during development gene; modifs chromatin, rendering heritable changes in neon expression; activates or | silences genes SURF-6; involved in a nucleolar Nucleolus (ubiquitous) ribosome | nousekeeping | i; mouse virus type | Wort10b; developmental Developing limbs, Tace and sail or regulation of cell growth and embryos and in adult differentiation in certain adult | mammalian tissues Citron; Rho (controls actin Ubiguitous structures) target protein; role in | int-2 (FGF-3); expressed in Early embryogenesis; discrete embryonic development regions during development; not reported in adult | Mitogen-activated protein kinase Liver parenchymal cells, vascular phosphatase 1/3CH134/ERP1); serum growth factor-induced immediate early |
|--|--|---|--|---|--|-------------------|------------------------|---|--|---|---|
| GenBank X16495 | U62669 | X56044 | | X56690 | X92842 | | X66285 | ET62229 | ET61747 | Y00848 | X61940 |
| std 0.11 | 0.13 | 0.21 | | 0.21 | 0.36 | | 0.60 | 0.14 | 0.22 | 0.45 | 0.17 |
| sw 1.36 | 1.19 | 1.16 | | 1.44 | 66.0 | | 0.82 | 0.00 1.54 | 1.11 | 1.12 | 1.08 |
| std 0.00 | 0.00 | 0.52 | | 0.48 | 0.47 | | 0.00 | 0.00 | 0.00 | 0.01 | 0.20 |
| 0.00 0.00 | | 0.30 | | 0.28 | 0.27 | | 1.11 0.17 0.00 | 1.09 0.27 0.00 | 0.00 | 0.00 | 0.47 |
| std 0.82 | 0.13 | 0.15 | | 0.11 | 1.51 0.35 | CYCLE / CEL | 0.17 | 0.27 | 0.58 | 0.38 | 0.17 |
| CR 1.22 | 1.07 | 1.11 | | 1.06 | 1.51 | | <u></u> | 1.09 | 1.66 0.58 0.00 | 1.93 | 1.46 |
| P CR | <0.001 1.07 0.13 | 0.034 | | 0.009 | 0.025 | PSOCEUROVOUEZICEU | 0.022 | 0.000 | 0.003 | 0.001 | 0.002 |

| Description gene; dephosphorylates MAP | kinase BTG3; negative control of cell Fibroblast, brain องศุล | C-abl; c-Abl; a nonreceptor Liver, B cells tyrosine kinase; appears to play a | role in cell cycle progression, cell proliferation and differentiation G1 cyclin-Cdk protein kinase Ubiquitous inhibitor p27, cell cycle; cyclin- dependent kinase inhibitor p27 | (Kip1) Phosphoinositide 3-kinase Liver (regulatory subunit p85alpha); plays critical roles in cell growth, | differentiation, survice, order vesicular transport Map Kinase Kinase (MEKK Ubiquitous 1); MEK kinases (MEKKs) are serine-threonine kinases that | regulate sequences and pathways involvable in mitogen-activated protein kinases (MAPKs), including members of the Jun kinase (JNK) family. Mitogen-activated protein kinase Liver (15 times higher in fetal than Mitogen-activated protein kinase Liver (15 times higher in fetal than Mitogen-activated protein kinase Liver (15 times higher in fetal than Mitogen-activated protein kinase Liver (15 times higher in fetal than mitogen-activated protein gould!); ubiquitous induced pedidermal growth factor; activation of MAPK induces c-Fos and c-Jun; CR reduces the age related decline in | MAPK activation Interferon-activatable gene (204); Nucleoi mediates |
|---|---|---|--|--|---|---|---|
| GenBank | 272000 | X07540 | U10440 | ET61628 | ET61257 | U85608 (was U11548) | M31419 |
| std | 0.20 | 0.16 | 0.45 | 0.21 | 0.23 | 0.22 | 0.39 |
| sw | 1.05 | 1.04 | 0.92 | 1.29 | 1.26 | 1.25 | 0.00 1.39 |
| std | 0.00 | 0.05 | 0.00 | 0.00 | 0.00 | 00.0 | |
| CON | 0.00 | 0.03 | 0.00 | 0.17 0.00 | 0.00 | 1.10 0.41 0.00 | 0.002 1.09 0.31 0.00 |
| std | 0.07 0.00 | 0.11 | 0.02 0.00 | 0.17 | 0.47 | 0.41 | 0.31 |
| cs S | 1.08 | 1.13 | 1.02 | 1.08 | 1.48 | | 1.09 |
| Q. | <0.001 1.08 | <0.001 1.13 0.11 0.03 | 0.006 | 0 | 0.002 1.48 0.47 0.00 | 0.002 | 0.002 |

-88-

| Description Location immunomodulary and cell growth-regulatory activities of interferons; increased up to 75-fold by alpha-interferon treatment and the contraction of the contraction o | Primase small (p49) subunit; cell Liver (ubiquicos) proliferation; DNA replication | (Xeroderma Pigmei A Correcting p ide excision DNA re | Brea gene; familial breast Ubiquitous cancer susceptibility gene; important in DNA double-strand | break repair (USBAN) and DNN call-cycle charage-induced cell-cycle checkpoint activation nuclear Ubiquitous protein, upregulated in response to UV and ionizing radiation; accumulated in the nucleus of | proliferating fibroblasts; proliferating inhibits overexpression into S phase MLH1; DNA mismatch repair Ubiquitous gene; function in mutation avoidance; cell cycle checkpoint control; cytotoxicity of various DNA-damaging agents; | excision repair. C.005 1.00 0.09 0.42 0.05 1.12 0.04 ET63241 Apopain protease; mediator of cysteine cysteine cysteine protease; mediator of cysteine cys |
|--|---|--|--|--|--|--|
| GenBank Lington | D13544 | X74351 | ET62746 | X58472 | ET63479 | 建化的 237110 ET63241 |
| std | 0.24 | 0.25 | 0.30 | 0.19 | 0.37 | 0.23 |
| Sw | 1.27 | 1.1 | 1.27 | 1.07 | 0.85 | 1.36 |
| std | 0.34 | 0.16 1.14 | 0.00 | 0.14 | 0.14 | 0.30 1.36 0.05 1.12 |
| CON | 0.48 | 0.45 | 0.00 | 0.13 | 0.17 | 0.33 |
| std | 1.36 0.37 0.48 | 1.24 0.37 0.45 | 1.03 0.29 | 0.13 | 1.02 0.03 0.17 | 3 <u>36日</u> 2013 0.33 1.07 0.19 0.33 1.00 0.09 0.42 |
| CR | 1.36 | 1.24 | 1.03 | 1.17 | 1.02 | 1.00 |
| P DNA | 0.029 | 0.025 | 0.001 | <0.001 1.17 0.13 | 0.00 | 5年10年105 5至30 |

-68-

| Description apoptosis; processes precurser IL-1; PARP-cleaning | Mdm2 is a P53 specific ubiquitin Liver ligase; promotes the ubiquitination and proteasome-dependent degradation of p53; immediately after cellular stress, MDM2 ability to bind to p53 is blocked, preventing MDM2-mediated degradation, P53 levels rise causing cell cycle arrest or apoptosis | a; Bcl-2-fam apoptotic actinets in lipid r | Bcl-2-beta; suppresses Liver programmed cell death | Zn-finger protein Pw1/Peg3; Ubiquitous activates NFkappaB; regulator of | TNF response; induced during p53/c-myc-mediated apoptosis; Pw1/Peg3 with Siah1a induces apoptosis independently of p53; inhibiting Pw1/Peg3 activity blocks p53-induced apoptosis. RNA-dependent EIF-2 alpha Ubiquitous kinase; double-stranded (ds) RNA-dependent protein kinase (PKR); ky mediator of antiviral | effects of interferon tilly, active player in apoptosis. Pt1, a novel gene related to ubiquitin-conjugating enzymes; Ft1, a novel gene related to ubiquitin-conjugating enzymes; deletion leads to partial syndactyly of the limbs and thyrmic deletion leads to partial syndactyly of the limbs and thyrmic hyperplassia, suggesting impaired programmed cell death | 建筑成成组织 BROWTH OTTEN SVIS GORD FOR THE STAND SANGLES STAND |
|--|---|---|--|--|---|--|---|
| GenBank | X58876 | L22472 | L31532 | U48804 | ET61211 | X71978 | VSF W.C. L. |
| std | 0.11 | 0.24 | 0.22 | 0.07 | 90.0 | 0.10 | 9 <u>ROTE</u> 0.09 |
| »s | 1.06 | 1.08 | 1.16 | 1.01 | 0.00 1.08 | 1.02 | 915 0.95 |
| std | 60.0 | 0.00 | 0.00 | 0.50 | 00.00 | 1,11 0,11 0.00 0.00 1.02 | 0.19 |
| CON | 0.05 | 0.00 | 0.00 | 0.47 | 0.19 0.00 | 0.00 | 1.28 0.19 0.11 |
| std | 0.13 | 0.15 | 0.28 | 0.15 | 0.0 | 0.11 | 360M3 0.19 |
| C. | 1.14 | 1.12 | 1.21 | 1.25 | 0.91 | 1.11 | 1.28 |
| ٥ | <0.001 1.14 0.13 | <0.001 1.12 0.15 0.00 | 0.001 | 0.050 | • | 0 | 0.000 |

-96-

| Description serum; synthesized by visceral endoderm of the yolk sac and by fetal liver; blood level decreases | in liver tumors Alpha-fetoprotein (AFP); main Liver (fetal & adult) component of mammalian fetal serum; synthesized by visceral endoderm of the yolk sac and by fetal fiver; blood level decreases after birth; synthesis reactivated in liver tumors | Serum amyloid A (Saa) 3; serum Liver protein; major acute phase | d A or, r | apolipoprotein); acute-phase apolipoprotein; induced by trauma and inflammation; normally rapidly catabolized; degraded by secreted or cell- associated neutral proteases | generated by macrophages Kallikrein; serine protease; Liver generates proinflammatory kinins; | Kallikrein-binding protein; tissue Liver, lung, thymus kallikrein segulation; serine proteinase inhibitor supermentations in proteinase inhibitor supermentations. | NATE OF THE TRANSPORT OF THE TRANSPORT OF THE STATE OF THE STATE OF THE TRANSPORT OF THE T | E-cadherin; cell-cell adhesion; cell Liver (epithelial cells) surface transmembrane protein |
|---|---|--|--------------|--|---|--|---|---|
| GenBank | M16395 | X03479 | ET63455 | | V00829 | X61597 | <u>ION的</u> Z50147 | X06115 |
| std | 0.16 | 0.26 | 0.35 | | 0.25 | 0.31 | 0.41 | 0.11 |
| »s | 1.07 | 1.30 | 1.71 | | 1.00 | 1.35 | 1.17 | 0.95 |
| std . | . 0.12 | 0.42 | 0.18 | | 0.25 | 0.00 | MATRIE 0.05 | 0.08 |
| CO | 0.07 | 1.14 0.13 0.38 | 0.57 | | 0.14 | 1,27 0,40 0.00 | <u>EEXTRACEBIULAR</u> 1.60 0.32 0.03 | 0.05 |
| std | 0.09 | 0.13 | 0.64 | | 0.50 | 0.40 | RACE 0.32 | 0.27 |
| 85 | 1.10 | 1.14 | 1.15 | | 1.57 | 1.27 | 1.60 | 1.34 |
| ۵. | <0.001 1.10 0.09 0.07 | 0.018 | 0.049 | | 0.008 | 0.002 | 0.002 | 0.000 1.34 0.27 0.05 |

-91-

| Description K-cadherin/cadherin-6; present at Cerebral cortex in neonatal mice; external cell surface at cell-cell newly formed epithelium of the renal | contact sites; calcium-dependent vesicle; proximal renal tubures, cell adhesion molecules CD4 + CD8 + thymocytes T2-cadherin; calcium-binding Thymocytes; developing testis and membrane glycoprotein; cell retina | adhesion molecule cadherin 11(cad11); calcium- Mesoderm surroundiny organs: dependent mesenchymal cell Developing somites; | adhesion molecule Vascular cell adhesion molecule-1 Liver (VCAM-I): immunoglobulin gene | Superfamily, transmissions of the control of the co | Collagen IV alpha 3 chain; Liver extracellular matrix; component | chain; × | Procollagen type V alpha 2 Liver Stromelysin 1; extracellular Liver, stromal cells matrix-degrading | metalloproteinase Tropoelastin; elastic fibers in Vessel vessel walls and other tissues consist of cross-linked | tropoelastin in association with several microfibrillar protein Plasminogen activator inhibitor 2; Liver; mainly expressed in the skin, serine protease inhibitor; bone-marrow, spleen, lung, thynus, inactivates urokinase-type and urinary bladder plasminogen activator and regulates degradation of the extracellular matrix; one form is cytoplasmic the other is |
|---|--|--|---|--|---|-------------|---|--|--|
| GenBank ET62381 | U69137 | X77557 | X67783 | 97699X | 235166 | 235168 | L02918 X66402 | U08210 | X16490 |
| std 0.14 | 0.05 | 0.34 | 0.34 | 0.19 | 0.34 | 0.36 | 0.39 | 0.43 | 0.13 |
| sw 1.26 | 1.06 | 0.99 | 1.17 | 1.22 | 1.32 | 1.51 | 1.42 | 1.46 | 1.15 |
| std 0.06 | 0.31 | 0.15 | 0.29 | 0.03 | 0.0 | 0.42 | 0.00 | 0.00 | 0.00 |
| CON 0.42 | 0.35 | 0.09 | 0.25 | 0.29 0.01 | 0.00 | 0.30 | 0.00 | 0.00 | 0.00 |
| std 0.16 | 0.09 | 0.13 | 0.22 | | 0.47 | 0.18 | 0.45 | 1.30 0.57 0.00 | 0.16 |
| 0.9 4 | 1.05 | 1.08 | 1.56 | 1.29 | 1.37 | 1.08 | 1.11 | | 1.12 |
| 9 0.001 | 0.006 | 0.003 | 0.004 | < 0.001 1.29 | 0.004 | 0.012 | 0.006 | 0.009 | <0.001 1.12 0.16 0.00 |

-95-

| Description translocated into the endoplasmic reticulum, glycosylated and | secreted Pancreatitis-associated protein Liver (ductular cells), pancreas, small pancreatitis-associated adhesion intestine protein; binds laminin; may be important in liver cell differentiation/proliferation; adhesion molecule for | hepatocytes Fibroblast activation protein; cell- Fibroblasts surface glycoprotein; member of the serine protease family; expressed at sites of tissue | Iduronato-2-sulfatase (IDS); Ubiquitous degrades heparin sulfate and dermatan sulfate in lysosomes; | disorder, attorage mucopolysaccharidosis type II (the glycosaminoglycans heparin sulfate and dermatan sulfate accumulate); part of proteoglycans which bind, help package and store secretory molecules; function in cell adhesion and basal lamina | formation MAINTENE STATE STATE STATE STATES | many types of cargo ARF3; ADP-ribosylation factor; Ubiquitous involved in formation of coated -93- |
|---|---|---|---|---|--|---|
| GenBank | D13509 | ET63188 | X75636 | | K <u>transponty (georetion martila elektronich mana</u> 0.010 1.15 0.14 0.31 0.37 1.09 0.16 ET63248 | . 087900 |
| std | 0.63 | 0.59 | 0.59 | | 5550 E | 0.15 |
| »s | 2,11 | 1.66 | 1.45 | | 1.09 | 1.15 |
| std | 0.29 | 0.23 | 0.00 | | 0.37 | 0.41 |
| CON | 1.21 0.41 0.32 | 0.46 0.13 | 0.00 | | ortakieoretions 1.15 o.14 o.31 | 0.99 0.16 0.25 |
| std | 0.4 | 0.46 | 0.70 | | 16 <u>ECR</u> 0.14 | 0.16 |
| S. | 1.21 | 1.31 | 1.61 | | PORTS/ 1.15 | 0.99 |
| ۵ | 0.010 | 0.014 | 0.017 1.61 0.70 0.00 | | K <u>ITRANSI</u> 0.010 | 0.013 |

-93-

| Description Location | Vesicle transport protein (munc-Ubiquitous 18c) | Alpha-adaptin; adaptor complex Liver and brain components; link clathrin to | coated vesicle receptors Rab 23; Ras-related small GTPase; Liver regeneration leads to protein trafficking; central differential regulation of some Rabs; regulatory elements of the other cells intracellular transport machinery; | regulate vesicle dockning end fusion, organelle dynamics Syntaxin 3A, IER vesicular Liver transport, membrane fusion | OA6; | and uterus; high levels of expression in epithelial lining the gastrointestinal, respiratory and | urinary tracts Serine proteinase inhibitor 6 Lymphocytes; endothelial and (SPI6); not secreted, remains in epithelial cells; platelets the endoplasmic reticulum; | intracellular function unclear N-acetylglucosaminyltransferase Liver III (Mgat3): transfers the bisecting GlcNAc to the core of | complex, N-linked carbonydates Rho kinase (p160, ROCK-2); Rho Ubiquitously expressed except in the is a small GTPase; brain and muscle serine/threonine coiled coil- | forming protein kinase; downstream targets include LIM- kinase 1, which phosphorylates cofilin, an actin-depolymerizing factor; regulates actin | .94- |
|----------------------|--|--|---|--|-----------------------|--|---|---|---|---|------|
| GenBank ' | U19521 | X14972 | 222821 | D29797 | X66449 | | 096700 | L39373 | U58513 | | |
| std | 0.12 | 0.13 | 0.17 | 0.45 | 0.11 | | 0.29 | 0.58 | 0.07 | | |
| SW | 1.12 | 1.06 | 1.04 | 1.28 | 1.13 | | 1.12 | 1.05 | 1.08 | | |
| std | 0.16 | 0.09 | 0.01 | 0.00 | 0.02 | | 0.00 | 0.00 | 0.11 | | |
| CON | 0.38 | 0.43 | 0.00 | 1.23 0.28 0.00 | 0.01 | | 1.21 0.18 0.00 | 1.10 0.15 0.00 | 0.97 0.15 0.48 | | |
| std | 1.04 0.07 | 0.15 | 0.07 | 0.28 | 0.09 | | 0.18 | 0.15 | 0.15 | | |
| 5 | 8. | 1.12 0.15 | 1.05 | 1.23 | 1.08 | | 1.21 | 1.10 | 0.97 | | |
| ۵ | 0.001 | 0.001 | <0.001 1.05 0.07 0.00 | 0.003 | <0.001 1.08 0.09 0.01 | | 0.001 | 0.013 | 0.001 | | |

| Location to to ti | transfer Ubiquitous ytosolic finositol between is gene intation) gressive stion of it cord | particle Ubiquitous pplasmic ssis and proteins | Polypeptide N- Wide expression pattern; detected in acetylgalactosaminyltransferase- embryonic tissues, as well as adult T4 (polypeptide GalNAc sublingual gland, stomach, colon, transferase-T4; ppGaNTase-T4); small intestine, lung, cervix, and fourth member of the mammalian uterus; lower levels detected in UDP-GalNAc; Golgi-like kidney, liver, heart, brain, spleen, localization; 4 GalNAc- and ovary transferase controls the initiation of mucin-type O-linked protein of mucin-type O-linked protein is acetylgalactosamine is serine and stansferred to serine and transferred to serine and | Carreticulin; endoplasmic reticulum chaperone; also functions in calcium storage and signaling, and cell attachment; nuclear matrix component | (IDS); Ubiquitous |
|--|---|---|---|---|-------------------------------|
| ation; Rho secretion; yosin light ay prevent activation | transfer cytosolic cytosolic cytosolic ylinositol between his gene nutationl ogressive ation of all cord. | art ass s · s | N-ransferase-GalNAc aNTase-T4); mammalian Golgi-like GalNAc-the initiation ked protein which N- is erine and | reticul | <u>e</u> |
| Description cytoskeletal reorganization; Rho activity enhances secretion; phosphorylation of myosin light chain and moesin may prevent pathologic platelet activation diving schannanesis. | phosphatidylinosical transfer phosphatidylinosical cytosolic protein alpha (Pitpol); cytosolic protein binds phosphatidylinosital and transfers it between membranes; mutant in this gene (the mouse vibrator mutation) causes an early-onset progressive action tremor, degeneration of brain stem and spinal cord | Signal recognition particle (SRP9); cytoplasmic ribonucleoprotein; synthesis and translocation of secreted proteins | Polypeptide acetylgalactosaminyltransferase- T4 (polypeptide GalNAc transferase-T4); ppGaNTase-T4); fourth member of the mammalian UDP-GalNAc; Golgi-like localization; 4 GalNAc-transferase controls the initiation of mucin-type O-linked protein glycosylation, in which N- glycosylation, in which N- garcetylgalactosamine and transferred to serine and transferred to serine and transferred acid residues | Calreticulin; endoplasmic calcium storage and signatrix component | Iduronato-2-sulfatase .95- |
| GenBank | U96724 | X78304 | ET62525 | X14926 | X75636 |
| pts | o.39 | 0.31 | 0.18 | 0.11 | 0.59 |
| ws ··· | 11. | 0.94 | 1.22 | 0.97 | 1.45 |
| std | 0.41 | 0.12 | 0.25 | 0.44 | 0.00 |
| CON | 0.24 | | .0 2. | 0.25 | |
| std | 0.56 | 0.13 | 0.08 | 0.06 | 0.70 |
| ಜ | 2.03 | 1.27 | 10.1 | 1.07 | 1.61 |
| ۵. | 00.00 | 0.001 1.27 0.13 0.07 | 0.001 1.01 0.08 0.15 | 0.017 1.07 0.06 0.25 | 0.017 1.61 0.70 0.00 |

| Description degrades heparin sulfate and deficiency causes fatal lysosomas; deficiency causes fatal lysosomal storage mucopolysaccharidosis type II (the glycosaminoglycans heparin sulfate and dermatan sulfate accumulate); part of proteoglycans which bind, help package and store secretory molecules; function in cell adhesion and basal lamina | formation <u>FIRANSIATION</u> (域景路)、建筑 <mark>建筑、建筑、建筑、建筑、建筑、建筑、建筑、建筑、建筑、建筑、建筑、建筑、建筑、建</mark> | homologue Ribosomal protein L7; Ubiquitous incorporated into 60 S subunit | Ribosomal protein L7 (rpL7); Ubiquitous incorporated into 60 S subunit | Ribosomal protein L32 Ubiquitous Signal recognition particle Ubiquitous (SRP9); cytoplasmic | ribonucleoprotein; synthesis and translocation of secreted proteins translocation translocations to the translocation of | 1) transcription factor ARE Binding Protein (AREC3) Many cell-types during development; muscle in adult | Sox12; transcription factor; Sox Developing embryos family plays important role in | development Pax2 transcription factor; paired Developing embryo excretory and box family (homologous to CNS | Drosophila segmentation genesi Putative transcription factor Many locations in embryo during | -96- |
|--|---|---|---|---|---|---|--|---|---|------|
| GenBank | 通过即长 近常 U28419 | X57960 | M29016 | K02060 X78304 | X74040 | ET61028 | ET62446 | X55781 | ET62078 | |
| Std. | 0.31 | 0.08 | 0.18 | 0.25 | 1765 1.1. 0.48 | | 0.46 | 0.18 | 0.09 | |
| % · . | 1.12 | 1.05 | 1.04 | 1.18 | 1820 136 136 136 136 136 136 136 136 136 136 | 1.08 | 0.77 | 1.14 | 1.26 | |
| std . | 0.28 | 0.00 | 0.29 | 0.00 | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 0.26 | 0.00 | 0.32 | 0.35 | |
| N 000 | 0.29 | | 0.37 | 0.00 | 18 C | | 0.00 | 0.39 | 0.50 | |
| std | (K)(R) | 0.24 | 0.22 | 0.05 | EION SE | 0.28 | 1.16 0.04 | 0.27 | 0.18 | |
| S. | ATTION! | 1.48 | 1.17 | 1.06 | SCRIP | 1.32 | | 1.19 | 1.16 | |
| <u>a</u> . | FERRISE | 0.000 | 0.013 | <0.001 0.001 | SOTE | 0.026 | 0.005 | 0.018 | 0.032 | |

| Location (tbx4); T-box DNA binding development domain; putative roll in inductive interactions | embryogenesis up-regulated Id4; CD44; dominant negative Embryogenesis, up-regulated regulators of bHLH transcription between day 9.5 and 13.5 of factors; differentiation in cellular gestation; adult highest expression systems including myogenesis, testis, brain and kidney; also in liver; and adipocytes, astrocytes, nuuscle cells haematopoiesis; | differentiation Zinc finger protein, the Kruppel-Liver, Iens, heart, kidney. spleen, associated box (KRAB); similar brain of newborn mice to profilaggrin (expressed in | differentiating epidernial cells) Neural-restrictive: silencer factor Many nonneuronal cells and tissues (NRSF/REST); transcription factor; represses expression of neuronal genes including mACHR, | SCG-10 and type in sociality channel genes; recruits mSin3 and histone deacetylase Zinc-finger protein Zfp-37; Liver transcription factor (putative); peroxisome proliferator resonnive: contains Kruppel- | associated box C-ros (c-ros); embryonic Neoplastic and fetal tissues development; tyrosine kinase catalytic domains; expressed in | neoplastic and fetal tissues Hox-7; transcription factor; early Embryogenesis stage of eye developmental | regulation in construction Embryogenesis Hox-1.7; homeobox; transcription Embryogenesis factor | Myf-5; myogen tactor 5; Embryome liver and reco97. |
|--|--|---|--|--|---|--|---|--|
| GenBank | X75018 | L28167 | U13878 | X89264 | U15443 | X59251 | M28449 | X56182 |
| std | 0.11 | 0.44 | 0.18 | 0.09 | 0.08 | 0.32 | 0.12 | 0.46 |
| SW. | 1.31 | 1.47 | 1.21 | 1.09 | 1.06 | 1.25 | 1.17 | 0.00 1.50 |
| std | 0.25 | 0.00 | 0.16 | 0.13 | 0.07 | 0.00 | 0.18 | |
| NO CO | 0.48 | 0.00 | 0.10 | 0.11 | 0.08 | 1.24 0.40 0.00 | 1.12 0.27 0.10 | 1.53 0.65 0.00 |
| std | 0.13 | 0.64 0.00 | 1,17 0.37 0.10 | 0.12 | 1.18 0.62 0.08 | 0.40 | 0.27 | 0.65 |
| CR | 1.06 0.13 0.48 | 1.56 | 1.17 | 1.09 | 1.18 | 1.24 | 1.12 | |
| ۵ | 0.003 | 0.009 | 0.003 | <0.001 1.09 0.12 | 0.018 | 0.003 | 0.001 | 0.01 |

| CR std CC 1.45 0.81 0. 1.23 0.23 0. 1.27 0.23 0. 1.56 0.52 0. 1.50 0.67 0. 1.08 0.17 0. 1.36 0.25 0. | std SW std GenBank | helix family .00 0.00 1.42 0.72 X13538 Hox-1.4; transcription factor Embryonic spinal cord and adult | 0.05 1,11 0.26 X60034 | 0.00 1.14 0.38 X80339 | .00 0.00 1.49 0.83 D00925 Transcription factor S-II-related Liver protein; transcription elongation | 0.22 0.88 0.27 X67719 | 0.00 1.34 0.29 X60136 | 0.15 1.02 0.07 X80508 | 0.00 0.95 0.13 X76858 | function; GLI-Kruppel function; GLI-Kruppel cell-cycle regulated 0.00 1.08 0.19 Y12783 Ring1B; interacts direction the repressor domain M33 is a transcript | in the | 0.29 1.41 0.32 X55315 | 0.00 1.02 0.04 X15842 |
|---|--------------------|---|-----------------------|-----------------------|---|-----------------------|-----------------------|-----------------------|-----------------------|---|--------|-----------------------|-----------------------|
| std CON 5 0.81 0.00 7 0.23 0.00 6 0.52 0.00 6 0.67 0.00 6 0.03 0.09 7 0.06 0.00 9 0.65 0.00 16 0.25 0.00 | | | | | | | | | | | | | 0.00 1.0 |
| std | | 0.00 | 0.03 | 0.00 | 0.00 | 0.13 | | | | 0.00 | | | 5 0.00 |
| | CR std | 1.45 0.81 | 1.23 0.23 | 1.27 0.23 | 1.56 0.52 | 1.17 0.15 | 1.50 0.67 | 1.16 0.03 | <0.001 1.07 0.06 | 1.99 0.65 | | 8 0.1 | 1.36 0.2 |

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| Description Alternative splicing factor (ASF); Ubiquitous (?) recruits basal splicing factors | during spliceosome CPEB protein; protein that interi maturation-type | polyadenylation element to promote polyadenylation and translational activation Srp20 gene; splicing factor Ubiquitous belonging to the highly conserved family of SR proteins; multiple roles in the regulation of constitutive and alternative | splicing I <u>MEMBRANE/PROTEIN WERNERSHORTSTORING TO THE STORING THE STORING TO THE STORING THE STORING TO THE STORING TO THE STORING TO THE STORING TO THE ST</u> | MHC class I T3-d gene; H-2-d Unknown haplotype; beta-2-microglobulin associated protein; cell surface | glycoprotein; class I antigen Major histocompatibility complex Ubiquitous DO beta gene | antigen 59-kd oncofetal antigen; Fetal antigen; not reported in adult antigen spresent on the surface tissues | tumors Connexin 43; gap junction Liver, heart, bone, skin, etc.; Mol proteins; contain ion exchange Carcinog 1996 Aug;16(4):203-12 channels that generate signals | throughout the tissue Connexin family of gap junction Ubiquitous (cell-to-cell channels) proteins (Cx50); likely 1S lens fiber protein |
|---|---|--|---|---|--|--|--|---|
| GenBank ET63161 | Y08260 . | X91656 | 欧州河沿河 M17376 | M75875 | J03298 | U90146 | X61576 | M91243 |
| std 0.10 | 0.07 | 0.44 | 0.51 | 0.37 | | 0.47 | 0.16 | 0.61 |
| SW 1.04 | 1.07 | 1.02 | 1.47 | 0.97 | 1.09 | 1.02 | 0.00 1.73 | 1.45 |
| std 0.33 | 0.26 | 0.00 | 00.0 | 0.00 | 0.38 | 0.00 | 0.00 | 0.00 |
| CON 0.38 | 1.04 0.12 0.15 | 1.14 0.19 0.00 | 00.00 | 0.00 | 0.10 0.44 | 1.76 0.14 0.01 | 1.07 0.73 0.00 | 0.024 1.41 0.69 0.00 |
| std 0.08 | 0.12 | 0.19 | OTEN 0.17 | 1.48 0.19 | 0.10 | 0.14 | 0.73 | 0.69 |
| CR 1.06 | 1.04 | 1.14 | 1.08 | 1.48 | 1.09 | 1.76 | | 1.41 |
| P 0.011 | 0.001 | 0.004 | MEMBRANEFROTEIN WARE | 0.001 | 0.036 | 0.001 | 0.008 | 0.024 |

| Location | itin; major Liver (ER) adaptor; the inverse elathrin to | proteins in icles in icles a Liver din located at tight junction to | neutral endopeptidase Ubiquitous CD10/NEP); cell surface roteinase; activation for mononuclear cells; | ed signal inactivates ous peptides , and lung in | vivo Apolipoprotein C2 (APOC2); Fetal liver, adult liver, intestine and required for lipolysis of peritoneal macrophages triglycerides by lipoprotein lipase | ha membrane ILA antigen | Glucose transporter 2 Cea14 gene (carcinoembryonic Many cea genes expressed in fetul antigen family members); liver | | the immunoglobulin superfamily Cea16 gene (carcinoembryonic Many cea genes expressed in fetal antigen family members); liver |
|------------------------|---|---|---|--|---|-------------------------------|--|------------------------------|--|
| nk Description MP70 | Gamma adap component of | | proteins CD10 24.11 (metallop marker | peptide mediated signal transduction; inactivates numerous endogenous peptides in the brain, kidney, and lung in | | | | the immi Cea15 antigen | |
| d GenBank | 40 X54424 | 0.38 U49185 | 0.37 M81591 | | 0.43 Z22216 | 0.27 V00834 0.21 X68061 | 0.36 M23383 0.12 ET63259 | 0.16 ET63260 | 0.28 ET63261 |
| std / | 0.40 | | | | | | | | |
| SW | 1.30 | 1.37 | 1.43 | • | 1.93 | 0.93 | 1.38 | 1.32 | 1.16 |
| std | 0.00 | . 00.0 | 0.13 | | 0.00 | 0.19 | 0.00 | 0.17 | 0.12 |
| CON | 0.00 | 0.00 | 0.60 | | 1.06 0.75 0.00 | 0.50 | 0.29 0.00 0.60 0.22 | 0.18 | 1.04 0.04 0.22 |
| std | 0.74 | 0.52 | 0.32 | | 0.75 | 0.03 | 0.29 | 0.15 | 0.04 |
| ខ | 1.38 | 1.43 | 1.28 | | 1.06 | 1.09 0.03 | 0.99 | 1.08 | |
| ۵ | 0.023 | 0.005 | 0.027 | | 0.009 | 0.026 | 0.002 0.038 | 0 | 0.001 |

| Description Location | unknown Tunction; member or the immunoglobulin superfamily the immunoglobulin superfamily | Glutamine; fructose-6-phosphate Liver amidotransferase (GFAT); rate- | limiting enzyme in hexosamine synthesis | CMP-N-acetylneuraminic acid Liver | nydroxyidse, gangilisase expression | Prostaglandin synthase Liver | cyclooxygenase Down in Ch Orotidine-5'-monophosphate Liver | | orotidine 5'-monophosphate to | Nat3 gene for N-acetyltransferase Liver | ACE; angiotensin-converting Liver | 16 | se | Thymidylate synthase (TS) Ubiquitous (all proliferating cells) | Alpha-galactosidase A; fysosomal Ubiquitous (most cases) | | -YE | glycogen digestion and | mobilization | S-nydroxy-S-illetinyigidatiy | enzyme for cholest | biosynthesis. | | Epithelial sodium chi subunit | AKR voltage-gated potassium-Ubiquitous channel (KCNA4) | Potassium channel gene (MK3) Ubiquitous | Putative capacitative calcium biant, signey, many constructions and constructions. | -101- |
|----------------------|---|--|--|-----------------------------------|--|------------------------------|---|------|-------------------------------|---|-----------------------------------|-----|--------|--|--|----------|--------|------------------------|--------------|------------------------------|--------------------|---------------|--|----------------------------------|---|---|--|-------|
| GenBank | NERGYZGEN | U00932 | | D21826 | | X98792 | M29395 | | | X72959 | J04947 | | L09105 | X14489 | U34071 | | J00355 | | | X0/888 | | | SALONICHANNEUS/PRIMPHYSICATION CHANGE CONTROLL C | ET61677 | U03723 | M30441 | ET61590 | |
| std | HCAASTE | 0.33 | | 0.21 | | 0.32 | 0.41 | | | 010 | 0.30 | | 0.13 | 0.80 | 0.51 | | 0.03 | | : | 0.19 | | | | 0.14 | 0.33 | 0.31 | 0.13 | |
| ΝS | e e e e | 1.34 | | 1.24 | | 1.58 | 1.42 | | | - | 20 | | 1.02 | 1.56 | 1.54 | | 1.11 | | | 1.20 | | | | 0.95 | 1.07 | 1.09 | 1.07 | |
| std | in Section 1 | 0.26 | | 0.41 | | 0.00 | 0.02 | | | 5 | 5 6 | ; | 0.08 | 0.00 | 8 | | 0.17 | | | 0.05 | | | | 0.00 | 0.34 | 0.34 | 0.13 | |
| CON | 100 C | 0.18 | | 0.33 | | 0.00 | 5 | | | 5 | | | 0.04 | | | | 0.51 | | | 0.29 | | | IMP | 0.00 | 0.35 | 0.45 | 0.13 | |
| std | (# d): | 0.05 0.18 | | 0.16 | | 0.31 | 20 | | | 6 | 3 5 | | 0 0 | 200 | | ! | 0.20 | | | 0.0 | | | IS://PI | 1.42 0.20 | 0.44 | 0.23 | 0.02 | |
| 85 | . 9 | 0.97 | | 1.10 | | 1.08 | , | 3 | | , | 5 . | - | 1 1 6 | | 3.7 | <u> </u> | 1.08 | | | 1.10 | | | PANNE | 1.42 | 1.33 | | 1.27 | |
| a | | 0.003 | | 0.016 | | 0.00 | 6 | 0.00 | | | 70.00 100.00 | 0.0 | 200 | 20.00 | 0.00 | 5 | 0.004 | | | 0 | | | SNOW | 0.000 | 0.044 | 0.039 | 0 | |

| | | 2 1 · | | | | pituitary. | | | | | | | |
|--|--|---|-------------------------|--------------------------------|---|---------------------------------------|--|-------------------------|--|--|--------------|--|---|
| iver | | Ne Ass | | | | brain, | | | | | | | |
| led in | | | | ve v | | liver. | y a | 2 | cells | | | | |
| detec | E | | | kid | ñ | nds. | , data | 2 | ithelial | | | sno | s no |
| Location message | dothel | iver | Liver Liver | il ie | | Sex glands, liver, brain, | | 200 | ver ep | ver | | biquito | biquito |
| Lo d in me to bled | 3; cation Endothelium or agonist- ve Ca2+ its of CCE | | Liver hormone Liver | factor | the tone | Š | | cell c | growth Liver epithelial cells actor-7 | ates Li by tion: | itory | interferon Ubiquitous ion of cell | cell |
| nvolved ndary s coup stein. | 3; cation agonist- e Ca2+ is of CCE | Sors | horn | factor | ber of | | | د ب ق | gro h fact | nd inactivates Jisted by | inflammatory | interf ition of | 1); gre ler |
| rp6); ir secor ceptors of G pre | protein 3; ssential for capacitative tive subunits | Tecepi | ceptor | ription | ; mem steroid | . 6 | | g growth (TGFbeta2); | grow1 | KGF) inds and inse up-regulated | <u>ئ</u> و | yte ; inhib | (type 1); helper |
| nnel (Trentry of reclass of | essent capa ative | E SE | coid re | transc | ARP-1) | eptors | | ing (TGF | on /te oblast | (mKGF binds: up- | 5 | leukocyte pha A); inhil | on beta T |
| Description entry channel (Trp6); involved in message detected in liver calcium entry secondary to activation of receptors coupled hy the Go class of G protein. | Trp-related protein 3; cation channel; essential for agonistative Ca2+ activated capacitative Ca2+ entry; putative subunits of CCE | channels <u>1950 in Recommendations of the Commentations of the Commentation of the Commentation of the Commentation of the Commentation </u> | Glucocorticoid receptor | receptor; transcription factor | Apolipoprotein regulatory protein (ARP-1); member of the COUP-family of steroid hormone | orphan receptors Androgen receptor | | Transform beta2 | proliferation Keratinocyte factor/fibroblast growth factor-7 | precursor (mKGF) Follistatin; binds and inactivates Liver activin; up-regulated by | • | castage Alpha leukocyte interferon (MulFN-alpha A); inhibition of cell | proliteration Interferon beta (type 1); growth Ubiquitous factor; T helper cell |
| Des entr calc | Cha acti | O 555 → | . . 9 5 | S & . | ğ g S | orp An | | Tra | | F 5 5 | ËÖ | | |
| GenBank | ET61440 | 医沟通性管理 X07751 | X04435 | | X76653 | X59411 | | 57413 | ET62118 | 229532 | | M28587 | V00755 |
| Ger | ET | | × 5 | ? | × | × | 37 | × | ᆸ | 7 | | Σ | > |
| std | 0.34 | 0.26 | 0.26 | <u>.</u> | 0.61 | 0.43 | | 0.45 | 90.0 | 0.40 | | 0.25 | 0.13 |
| »s | 1.43 | 開設調 | 1.23 | = | 1.21 | 1.40 | ANT N | 1.61 | 1.05 | 0.94 | | 0.94 | 1.04 |
| std | 0.10 | | 0.16 | 0.02 | 0.00 | 0.04 | ORES | 0.18 | 0.32 | 0.00 | | 0.17 | 0.35 |
| N O O | 90.0 | SHS (M) | | 0.03 | 0.00 | 0.35 | HEACT | 0.11 | 1.11 0.23 0.35 | 1.38 0.08 0.00 | | 0.11 | 1.31 0.23 0.44 |
| std | 0.35 | CEPTO | | 0.23 | 0.12 | 0.00 | TWO P | 0.23 | 0.23 | 0.08 | | 0.13 | 0.23 |
| ద్ | 1,19 0.35 0.06 | ARTE | 1.38 | 1.20 | 1.13 | 06 | Politicity (| 1.10 0.23 0.11 | | 1.38 | | 1.41 | |
| a . | 0.002 | ESTAUCIEARTRECEPTORS WALKS DESTABLE TO SE X | 0.003 | < 0.001 | 0.01 | 940 | ENGLISHED BY THE ACTORISM TO THE SECOND TO | 0.003 | 0.012 | 0.001 | | 0.000 1.41 0.13 0.11 | 0.015 |

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| | s (vascular); pituitary; mesothelial cells; cocytes | I cells, olfactory ura, septum, | thymus, heart. as, splecn, kidney. | | sxpressed in many g liver) during ment | lendothelial cells. |
|--------------------------------|---|--|---------------------------------------|--|--|--|
| Description factor; antiviral; | Endothelial cell peritoneal astrocytes; leul | factors, angiogenic factor; levels are markedly elevated after liver injury; stimulates hepatocyte proliferation and migration at the wound front; NT-3 gane for neurotrophin-3; Liver parenchymal cells, nared in the high bulb, cerebollurn, | camp ragm, ial | of TGF-beta superfamily Inhibin beta-B subunit; activins Liver are dimeric proteins, members of the transforming growth factor | beta (TGF-beta) gene superfamily, consisting of beta- subunits of inhibin (betaA and betaB) C-fos-induced growth factor Endothelial cells, expressed in many (FIGF); secreted dimeric protein tissues (including liver) during member of the platelet-derived embryonic development growth factor/vascular endothelial growth factor POGFIVE Family; mitogenic | fibroblasts. Preproendothelin-1; induces Vascular wall (endothelial -103- |
| GenBank | M30644 | X53257 | J00424 U96386 | X69620 | X99572 | U07982 |
| std | 0.16 | 0.21 | 0.23 0.38 | 0.39 | 0.55 | 0.22 |
| SW | 1.15 | 1.12 | .13 | | 6.1 | 0.26 1.17 |
| std | 0.17 | 0.15 | 0.17 | 0.00 | 0.32 | |
| 0 0 0 | 1.10 0.10 0.48 | 0.09 | 1.07 0.07 0.10 | 0.00 | 0.18 | 0.003 1.11 0.10 0.26 |
| std | 0.10 | 0.0 | 0.07 | 1.24 0.41 | 2.25 0.40 | 0.10 |
| చ | | 1.12 | 1.07 | | | 1.11 |
| ۵ | 0.002 | < 0.001 1.12 0.04 0.09 | 0.00 | 0.001 | 0.003 | 0.003 |

| CON std SW std GenBank Description Location Smooth muscle alpha-actin arterial smooth muscle cells, select expression; induced in stellate epithelial cells); kidney, lung, and endothelial cells of liver after trachea; liver (nonparenchymal cells, injury endothelial cells) endothelial cells) endothelial cells) | Stathmin; Stathmin Stathmin Stathmin; Stathmin | other activities N-ras; key component of growth Liver, wide tissue distribution signaling pathways; transmits membrane receptor kinase signals; GTP-binding switch | protein Mitogen-activated protein kinase Liver parenchymal cells, vascular Mitogen-activated protein kinase Liver parenchymal cells, vascular 1908-14-14-15-15-15-16-16-16-16-16-16-16-16-16-16-16-16-16- | sine plated to inase vi mitos | Aspergillus nidulans) Ras-GTPase-activating SH3- Ubiquitous domain binding protein (G3BP); assential for Ras signaling | G protein beta-subunit Brain, liver, blood cell G protein alpha i 1 subunit Liver; cerebral cortex; pancreatic acinar cells; white adipose tissue; | SUMO-1 activating enzyme Ubiquitous -104- |
|---|--|--|---|-------------------------------|--|--|--|
| GenBank (| X82320 X82320 | X13664 | X61940 | S45828 | U65313 | M63658 U38501 | AA162130 |
| pts | 0.19 | 0.40 | 0.17 | .0.15 | 0.22 | 0.57 | 0.11 |
| NS . | 1.09 | 1.13 | 1.08 | 0.00 1.09 '0.15 | 1.23 | 1.02 | 1.06 |
| std | 0.29 | | 0.20 | 0.00 | 0.15 | 0.00 | 0.41 |
| N CO S | 0.30 0.30 | 0.41 | 0.47 | 0.00 | 0.10 | 0.00 | 0.24 |
| std | <u>Seve</u> 0.21 | 0.25 | 0.17 | 0.48 | 1.09 0.27 | 1.02 0.03 1.09 0.11 | 1.32 0.28 |
| ម | <u> 1.30 0.21 0.30</u> | 1.19 | 1.46 0.1 | 1.17 | 1.09 | 1.02 | 1.32 |
| ۵ | # <u>\$SIGNAYETRĀNĒBŪ</u> 0.004 1.30 0.2 | 0.041 | 0.003 | 0.004 | 0.001 | 0.013 | 0.010 |

| Description subunit 1 (SAE1): one subunit of a dimer that conjugates SUMO-1 (a small ubiquitin-like protein) to other proteins; SUMO-1 modification of 1 Kappa B alpha takes place on the same residues used for ubiquitination; blocks NF kappa B-dependent transcriptional | activation Phospholipase C gamma 1; Ubiquitous; hepatocytes; hepatic substrate of many growth factor stellate cells; vascular smooth receptor and nonreceptor tyrosine muscle; vascular endothelial cells kinases; produces second messenger molecules that are elements of signal transduction pathways related to cell | proliteration. Rho kinase (p160, ROCK-2); Rho Ubiquitously expressed except in the is a small GTPase; brain and muscle serine/threonine coiled coil-forming protein kinase; downstream targets include LIM-kinase 1, which phosphorylates cofilin, an actin-depolymerizing factor; regulates actin cytoskeletal reorganization; Rho activity enhances secretion; phosphorylation of myosin light chain and moesin may prevent pathologic platelet activation during atherogenesis. | Map kinase kinase kinase (MEKK 1); serine-threonine kinase; regulates sequential protein phosphorylation pathways involving mitogen-activated protein kinases (MAPKs), including some Jun | Kinases Mitogen-activated protein kinase Liver (15 times higher in fetal than (MAPK); signal transduction; adult); ubiquitous |
|---|--|---|---|---|
| GenBank | ET63005 | U58513 | ET61257 | U85608 (was |
| std | 0.55 | 0.07 | 0.23 | 0.22 |
| % | 2.16 | 1.08 | 1.26 | 1.25 |
| std - | 00.0 | 6.0 | 0.00 | 0.00 |
| CO | 00.00 | 0.48 | 0.00 | 1.10 0.41 0.00 |
| std | 0.50 | 0.15 | 0.47 | 0.41 |
| 85 | 1.11 | 0.97 | 1.48 | |
| a. . | 0.003 1.11 0.50 0.00 | , | 0.002 1.48 0.47 0.00 | 0.002 |

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| | | | sen (ubiquitous) | s, broad tissue | | |
|--|--|---|---|---|---|----------------|
| Description important in cell proliferation, differentiation, and apoptosis; | induced by epidermal growth factor; activation of MAPK induces c-Fos and c-Jun; CR reduces the age related decline in MAPK activation Smad5; Liver | downstream components in TGF-beta family signaling cascade, transduces signals from the cell surface to the nucleus; participates in regulation of gene expression; essential in left/right isomerism and liver development; essential for anglogenesis | Histamine H1 receptor; GTP- Liver, brain, spleen (ubiquitous) binding protein-coupled roceptor; coupled to phosphoinositide turnover-calcium mobilization signaling pathway; regulates insulin-like growth factor I | expression and cell proliteration; modulates IL-6 action; regulates physiological functions in neurons; regulates transport of thyroxina into hepatocytes k; antinen (PA28 qamma); cell Liver, neurons, | proliferation; the interferon distribution gamma (IFN-gamma)-inducible PA 28 activator complex enhances the generation of class I binding peptides by altering the cleavage | |
| GenBank U11548) | ET62570 | | D50095 | 060031 | | M31419 |
| std | 0.32 | | 0.27 | | | 0.39 |
| SW | 0 | | 1.18 | | د. د | 1.39 |
| std | . 0.20 | | 0.00 | | 0 | 0.00 |
| CON | 0.12 | | 0.00 | | 1.09 0.16 0.00 | 1.09 0.31 0.00 |
| std | 0.08 0.12 | | 1.24 0.31 | | 0.16 | 0.31 |
| చ | 1.09 | | 1.24 | | 1.09 | |
| ۵. | 400 | | 0.001 | | 0 | 0.002 |

| | | | | inuscle | | | | | | | | brain; | |
|-------------|--|--|---|--|---|--|------------------------------|-----------------------------------|-----------------------------------|--|--|--------------------------------|---------------------------------------|
| | | Marie Commence | | smooth | | | | | | | row | muscle, | |
| | | 经位置的条件 | | receptor Neurons, vascular smooth inuscle as both cells w been | | | | | xpressed | iquitous) | l bone mar | liver, | |
| Location | | Liver | | r Neurons, cells | | 7 | | | G- Widely expressed tor; | ; Liver (ub e n | n y Liver and d g e | (OB-R); Lung, | |
| Ha? | activities of ed up to 75- | Treatment | de (NPYR-D) | recepto to as both | literature) de Y is ar of energy | genic, and actions; y in the | tem); NP) | is including | ā | clase e receptor; membrane modulation | ie protein ; primary cell-derived stimulating smembrane | (0B-R) | |
| | ulary a latory act increased | interferon | neuropepti Y receptor | upled e Y (referred to the pass) | as Y6 in neuropepti regulator mammals | antithermo cretagogue abundanti | vous syst | il response | | idenylyl cyl B1 subtyp -coupled tininogen | acute phase protein s ne receptor; primary stromal cell-derived e-B growth stimulating | ptor receptor | |
| Description | immunomodulary and congrowth-regulatory activities of interferons; increased up to 75- | fold by alpha-interferon treatment Marketing Control Liver Liver | raincreaus polypeptide/neuropeptide Y/peptide YY receptor (NPYR-D); | G protein-coupled Neuropeptide Y receptor Neuro Y5/Y6/Y2b (referred to as both cells | designated as (New Tope in literature); (NPY-Y6); (neuropeptide Y is an important regulator of energy important regulator through its | orazioni, antithermogenic, and insulin secretagogue actions; expressed abundantly in the | central nervous system); NPY | physiological responses including | Melanocortin 5 protein-coupled | stimulates adenylyl cyclase Bradykinin B1 subtype receptor; Liver (ubiquitous) G protein-coupled membrane bound; T-kininogen modulation | during acute phase protein synthesis Chemokina receptor; primary Liver and bone marrow receptor stromal cell-derived factor/pre-B growth stimulating factor, seven transmembrane | domain receptor Leptin rece | -107- |
| GenBank [| æ Gr.= | HANNENERICERTORS STATE S | 991040 | U58367 P | . 00.2 | | | | X76295 | ET61559 | X99581 | ET61693 | |
| std | | | 9.43 6.43 | 0.10 | | | | | 0.32 | 0.82 | 69.0 | 0.10 | |
| SW | | | 1.39 | 1.15 | | | | | 0.95 | 1.29 | 1.38 | 0.98 | |
| std | | | 0.38 | 0.03 | | | | | 0.34 | 0.00 | 0.16 | 0.22 | |
| CON | | ORS | 0.33 | 0.02 | | | | | 0.31 | 0.60 0.00 | 0.64 0.17 | 0.38 | |
| std | | ÉCÉŘI | 1,11 0.15 0.33 | 1.00 0.15 | | | | | 1.12 0.15 | 0.60 | 0.64 | 0.18 | |
| 8 | ; | KANER | 1.11 | 1.00 | | | | • | 1.12 | 1.89 | 2.14 | 1.46 | |
| a | | N.MEMBI | 0.029 | 0 | | | | | 0.027 | 0.020 | 0.013 | 0.001 1.46 0.18 0.38 | · · · · · · · · · · · · · · · · · · · |

| Description Location transmembrane receptor developing bone, mesenchyme, notochord and liver (Am J Clin Nutr 1999 Jan;69(1):18-21) | Macrophage inflammatory MIP-1alpha RL2 in liver and spleen protein-1 alpha receptor; mediates growth inhibitory | effects of the chemowing CD44; receptor for hyaluronan; Liver, central nervous system, lung. CD44; receptor for hyaluronan; liver epidermis, and pancreas hyaluronan clearance from the hyaluronan clearance from the hyaluronan clearance from the hyaluronan clearance. | homing and activation; BEK fibroblast growth factor Li + J520 liver parenchymal cells and receptor (BEK FGF receptor, FGF- others 2), membrane-spanning tyrosine kinase; activated by three | members of the FGF family; activation causes the foregut endoderm to develop into the | Member of the macrophage Widespread tissue distribution; fotal mannose receptor type C liver; endothelialized sites; mannose receptor type C liver; endothelialized sites; (calcium dependent) tectin family; chondrocytes in cartilaginous regions critical for processes ranging of the embryo from cell adhesion to antigen presentation; gene family includes macrophage mannose, the phospholipase A2, and the | Macrophage colony-stimulating Liver factor-1 (CSF-1) receptor | Ryanodine receptor type 2; form ER; cardiac muscle; neurons; most Ca2 + channels in the membrane excitable cells; liver of the ER; intracellular calcium release channels controlling | cytosolic carcium leveis. Transferrin receptor; cell surface Liver | -108- |
|--|---|---|---|---|---|---|---|---|-------|
| GenBank | U28404 | U57612 | M86441 | | U56734 | X06368 | X83933 | x57349 | |
| std | 0.19 | 0.12 | 0.24 | | 0.20 | 0.38 | 0.34 | 0.31 | |
| SW | 0.97 | 1.12 | 1.28 | | 1.13 | 1.27 | 1.21 | 1.23 | |
| std | 0.00 | 0.29 | 0.00 | | 0.00 | 0.11 | 0.03 | 0.00 | |
| CON | 0.00 | 0.48 | 0.00 | | 00.0 | 0.15 0.06 | 0.02 | 1,19 0.38 0.00 | |
| std | 0.10 | 0.20 | 0.25 | | 0.05 | 0.15 | 0.15 | 0.38 | |
| 8 | 1.52 | 1.10 0.20 0.48 | 1.24 | | 1.04 | 1.17 | 1.13 | 1.19 | |
| ۵ | 0.000 1.52 0.10 0.00 | 0.017 | <0.001 1.24 0.25 0.00 | | < 0.001 1.04 0.05 | 0.002 | 0.001 | 0.003 | |

| | | | tissue | | | | nd brain) | | | | d soinal | n heavy n-storing | cells) of | vy chain | ing cells tells) of | 9 | g liver: | enithelial | | |
|---|---|--|--|---|--|--|--|---|-----------------------------------|---|-----------------------|---|---|---|---|--------------------|--|------------|--|-------|
| | | | broad | | | | nly liver a | | | | na eiloo | al myosi sed in fa | ss, or Ito | yosin hea | in fat-storing cells or Ito cells) of | , , | regenerating liver; | theliam | | |
| Description Location hydroprotein: cell growth; binds | the major serum iron-transport protein, transferrin, and mediates | cellular iron uptaka P2X purinergic receptor (P2XR) Liver; ubiquitous channels bind extraacellular ATP | and mediate Ca(2+) influx Ki antigen (PA28 gamma); cell Liver, neurons, | gamma (IFN-gamma)-inducible PA 28 activator complex enhances | the generation of class I binding peptides by altering the cleavage | pattern of the proteosome or period of the proteosome filled the proteosome of the p | NF-M gene for middle-molecular-Epithelial cells (mainly liver and brain) mass neurofilaments (like | keratins) Formin: representization of the Ubiquitous | cytoskeleton, cytokinesis, stress | fiber formation, and transcriptional activation of the | serum response factor | Myosin heavy chain gene, nover Cha, "cpitain, gangin, mayosin heavy and unique C-terminal region ganglia; Ild skeletal myosin heavy chain gene expressed in fat-storing | cells (FSC, lipocytes, or Ito cells) of | regenerating liver Noomuscle myosin heavy chain CNS; IId skeletal myosin heavy chain | IIB; cell motility gene expressed in (FSC, lipocytes, | regenerating liver | Myosin light chain 2; contractile fat-storing cells (FDC, lipocytes, or notein) of regenerating liver. | | Epidermal keratin subunit; Liver (uile doct ep | -109- |
| GenBank | | X84896 | 060330 | | | | X05640 | ET 62211 | - 1077 | | | X57377 | | ET61336 | | | M91602 | | 00830 | |
| std | | 0.03 | 0.13 | | | | 1.35 | 9 | 2 | | | 0.51 | | 3 | 25.0 | | 0.31 | | 0.35 | |
| SW | | 1.10 | 1.15 | | | | 1.60 | | 5. | | | 1.41 | | • | 77: | | 1.12 | | 0.97 | |
| std | | 0.00 | 0.00 | | | | 0.00 | 6 | 0.23 | | | 0.00 | | Ċ | 0.20 | | 0.00 | | 0.00 | |
| CON | | 0.00 | 0.00 | | | | 0.20 0.00 | | 0.40 | | | 0.00 | | | 0.38 | | 0.00 | | 9.0 | |
| std | | 0.26 | 0.16 | | | | 0.2 | | 0.19 | | | 0.83 | | | 0.07 | | 0.35 | | 0.15 | |
| ຮ | | | 1.09 | | | ECETION | | | 1.07 0.19 | | | 1.42 0.83 | | | 1.06 0.07 | | 1.62 | | 1.90 0.15 | |
| ٥. | | <0.001 0.98 | 0 | | | CYTOSKEĽE! | 0.022 | | 900.0 | | | 0.033 | | | 0.012 | | 0.001 | | 0.000 | |

| Description Intermediate filament protein; cells | maintenance of epidermal cell shape and resistance to mechanical trauma Rho kinase (ROCK-2); (Rho is a Ubiquitously expressed except in the small GTPase; serine/threonine brain and muscle protein kinase); Rho activity enhances | phosphorylation of myosin light chain Chain Microtubule-associated protein 4 Most cell types including liver (MAP4); co-localizes with microtubules; expressed during developmental; likely involved in | GRIEGERSCHEIN STANDEN STEIN STEIN STANDEN STEIN ST 0.006 1.12 0.23 0.35 0.30 1.33 0.19 X97719 Friend-virus-susceptibility-1 gene (Fv1); prevents or delays spontaneous or experimentally induced viral tumors | Neurofibromatosis type 2 gene; Ubiquitous tumor supressor gene; Cytoskeleton-membrane linker; | mutant leads to CNS tumors RNA-dependent EIF-2 alpha Ubiquitous kinase; double-stranded (ds) RNA-dependent protein kinase (PKR); key mediator of antiviral | player in apoptosis. Minimum Company of the compan | female cell, and also inactive on the Y of male cells WW domain binding protein 6; Uncharacterized WW domain is a globular protein | -110- |
|---|--|--|---|---|--|--|---|-------|
| GenBank [| U58513 P | ET61218 (| X97719 | X74671 | ET61211 | X96737 | ET62791 | |
| std | 0.07 | 0.20 | RSFAAN 0.19 | 0.39 | 90.0 | 0.16 | 0.22 | |
| SW | 1 .08 | 1.32 | PRESSO 1.33 | 3.00 | 1.08 | 1.13 | 1.21 | |
| std | 0.11 | 0.02 | MORISU 0.30 | 0.00 | 0.00 | 0.00 | 0.00 | |
| CON | 0.48 | 0.47 0.49 | 0.35 | 1.77 1.69 0.00 | 0.0 | erioid - Frank Nown - Art - S. S. 1.23 0.24 0.00 | 0.59 0.00 | |
| std | 0.15 | 0.47 | 0.23 | 1.69 | 0.19 | 0.24 | 0.59 | |
| S | 0.97 | 0.97 | 改 题 1.12 | 1.77 | 0.91 | KEUNETION JUNKNOWN 0 1.23 | 1.35 | |
| ۵. | 0.001 | 0.038 | 0.00e | 0.029 | 0 | REFERENCIAL PROPERTY OF THE CONTROL OF T | 0.007 | |

CR std CON std SW std GenBank Description Location domain that is involved in mediating protein-protein interaction and that ultimately participates in various intracellular signaling events; WW domain mediates protein-protein interaction by binding proline-rich modules in ligands.

-1111-

APPENDIX B

| Name/Description Homeobox-containing protein (Hox-Most abundant in 12-day-old Homeobox-containing protein (Hox-Most abundant in 12-day-old embryos and progressively 1.11) decreases during further embryonic development. | gene ndant script ormal to rental the the being | inherited gene being repressed. Selenoprotein P: covalently bound Liver, testis, brain, gut, and 8-12 selenocysteine residue. Its hematopoietic cells concentration is sensitive to the selenom status of the animal. Its | Gelsolin: a Ca2+- and Ubiquitous Gelsolin: a Ca2+- and Ubiquitous polyphosphoinositide 4,5- bisphosphate (PIP2)1-regulated actin filament severing and capping protein that is implicated in actin | remodeling in growning and in apoptotic cells Fragile X mental retardation Brain syndrome protein (Fmr1) (mouse homologue): Fragile X Mental homology, Syndrome is the most | retardation, and is caused by defects in the FMR1 gene. FMR1 is an RNA-binding protein and the syndrome results from lack of |
|--|---|--|--|---|--|
| GenBank P M95599 P | X58196 | X99807 | J04953 | L23971 | |
| s std 0.28 | 0.28 | 0.05 | 0.16 | 0.58 | |
| Sw-ave 0.73 | 0.91 | 0.79 | 0.75 | 0.33 | |
| std 0.06 | 0.27 | 0.46 0.79 | 0.80 0.75 | 0.53 | |
| Low-Hi-Low p value CR-ave. std Cont-ave std Sw-ave std p.001 0.77 0.20 1.84 0.06 , 0.73 0.20 | 1.85 | 0.23 2.14 | 1.26 4.28 | 0.78 1.96 | |
| std 0.20 | 0.04 1.85 | 0.23 | 1.26 | 0.78 | |
| Low CR-ave. 0.77 | 0.54 | 0.89 | 1.17 | 0.68 | |
| Low-Hi-Low p value CR- 0.001 0.7 | 0.001 0.54 | 0.002 0.89 | 0.005 1.17 | 0.044 | |

| Name/Description Expression of FMR1 or expression of a mutant protein that is impaired in RNA binding. The specific function of FMR1 is not known | Mouse protein kinase inhibitor Testis specific (testicular isoform): inhibitor protein of the MMP-dependent protein vinase This isoform of PKI is | reported found only in testis High-glycine tyrosine keratin type Hair II.3 | DNA for y, Blood genes, bh2 | and bus pseudogenes. EN-7: Thas 100% seq homology T, B and myeloid hemopoictic with RAS-related C3 botulinum cells cubstrate 2 (Rac2)]: a member of | the ras gene superfamily. mRNA expression is restricted to the cells of hemopoietic. lineages, mRNA levels increase with the terminal differentiation of hemopoietic cells into granulocytes. Mannose-binding protein A (MbI1):a Blood serum protein, a member of a family of collagenous. lectins (collectins), that activates the complement system after binding to | glycoconjugates found on the surface of microorganism Mouse complement C1q B chain: Macrophages Mouse complement component C1q |
|---|---|--|-----------------------------------|---|---|---|
| GenBank | L02241 | D89901 | X14061 | X53247 | U09010 | M22531 |
| std | 0.00 | 0.26 | 0.42 | 0.37 | 0.18 | 0.38 |
| Sw-ave std | 8.02 0.00 | 0.16 | 1.23 | 0.98 | 0.61 0.94 | 0.95 1.21 |
| bts . | n, blood 8.02 | 1.85 | 0.34 | 1.00 | 0.61 | 0.95 |
| Cont-ave std | <u>Not reported in liver, muscle, brain, blood:</u> 0.032 0.18 0.31 11.84 8.02 (| 1.37 4.54 | <u>गीड</u> 0.12 2.89 | 3.06 | 0.13 2.15 | 0.05 2.55 |
| std | <u>iver, ਸ਼</u> 0.31 | 1.37 | ells 0.12 | 0.27 | 0.13 | 0.0 |
| Low-Hi-Low p value CR-ave. std | orred in 1 0.18 | 1.24 | Blood, T and B cells 0 0.77 0. | 0.29 | 0.79 | 0.72 |
| Low-Hi-Low p value CR-: | <u>Not reported in</u> 0.032 0.18 | 0.017 1.24 | Blood | 0.004 | 0.008 | 0.022 |

| Name/Description is a serum glycoprotein which is a serum glycoprotein which consists of six A chains, six B chains and six C chains. | Lactate dehydrogenase-A (LDH-A) Liver, muscle Lactate dehydrogenase A4 Liver, muscle isoenzyme Hexokinase(HK): catalyzes the first Liver, muscle | step in glucose metabolism, that 1s, the conversion of glucose to glucose-6-phosphate (G6P) Hepatic triglyceride lipase: an Liver important enzyme that is involved in the metabolism of chylomicrons, | intermediate density lipoproteins, and high density lipoproteins CTP-phosphocoholine cytidylytransferase: Phosphatidylcholine (PC) is the most abundant eukaryotic phospholipid and serves critical structural and cell-signaling functions. | CTP:phosphocholine cytidylyltransferase (CT) is the rate-limiting enzyme in the CDP-choline pathway of PC biosynthesis, which is utilized by all tissues and is the sole or major PC biosynthetic pathway in all non-hepatic cells | Fibronectin (FN): an extracellular Ubiquitous? matrix protein, is involved in the adhesion and migration of hematopoictic cells, found in many |
|---|---|--|--|--|--|
| GenBank | Y00309 X02520 J05277 | X58426 | U84207 | | M18194 |
| std | 0.26 | 0.33 | 1.77 | • | 0.22 |
| Sw-ave std | 0.90 | 0.79 | 1.17 | | 0.67 1.02 |
| `- | 0.75 0.90 1.18 0.73 | 0.88 0.79 | 12.59 1.17 | | 0.67 |
| Cont-ave std | Energy Metabolism / Biosythesis 0.006 0.85 0.15 2.57 0.018 0.97 0.15 2.87 | 0.07 2.10 | 0.00 43.66 | | ix 0.17 2.32 |
| | 0.15 0.15 0.15 | 0.07 | 0.00 | | 0.17 |
| Low-Hi-Low p value CR-ave. std | Metabolis 0.85 0.97 | 0.92 | 0.00 | | Extracellular Matrix 0.009 0.83 0 |
| Low-Hi-Low p value CR- | 6.006 0.006 0.018 | 0.008 | 0.001 | | <u>Extrace</u> 0.009 |

| Tissue | an Ubiquitous all is int ein ind | Ubiquitous? | Ubiquitous | Liver, adipose, brain kidney, lung, spleen, small intestine. |
|--|---|--|--|--|
| Name/Description extracellular matrices as well as being abundant plasma proteins. The plasma isoforms of fibronectin, which are synthesized in the adult by liver hepatocytes, differ from those derived from most other cells and tissues due to alternative mRNA splicing | Polyubiquitin: Ubiquitin is omnipresent protein found in eukaryotes so far analysed. It involved in several import processes, including proturnover, chromosome structure a stress response | Proteasome subunit MC3 (alpha Ubiquitous? type): The proteasome is a multisubunit 20 S proteinase complex involved in ubiquitin- | dependent and independent intracellular protein metabolism. ADP-ribosylation factor 2 (ARF2) Ubiquitous ADP-ribosylation factors (ARFs) are a family of small GTP-binding proteins that are involved in the formation of coated transport | vesicles for protein secretion through the endoplasmic reticulum and Golgi vesicular trafficking system Glucose-regulated protein 78 |
| GenBank | ET 6 1037 | X70303 | D87899 | D78645 |
| pıs | 0.38 | 0.06 | 3.98 | 0.29 |
| Sw-ave std | 1.13 | 0.98 | 2.78 | 1.71 1.01 |
| pts . | 0.25 1.13 | 0.33 | 3.18 | 1.7.1 |
| Cont-ave std | Protein Turn-Over / Itansport / Processing 0 0.83 0.02 3.40 0.25 0.25 | 0.12 2.11 | 0.00 16.01 | 0.17 3.06 |
| . std | <u>er / Tra</u> 0.02 | 0.12 | 0.00 | 0.1 |
| CR-ave | 0.83 | 0.73 | 0.00 | 0.81 |
| Low-Hi-Low p value CR-ave. std | Protein '0 | o | 0.001 | 0.063 |

| GenBank Name/Description Tissue | M13964 Stimulatory G protein of adenylate Ubiquitous cyclase, alpha chain: component signal transduction systems. | Peroxisome proliferator activated Liver receptor alpha: is activated by a diverse class of rodent hepatocarcinogens that causes proliferation of peroxisomes |
|---|---|--|
| GenBank | | X57638 |
| std | 0.09 | 0.24 |
| Sw-ave | 0.57, '0.83 | 0.85 0.82 |
| std | 0.57 | 0.85 |
| Cont-ave | | 2.14 |
| Low-Hi-Low p value CR-ave, std Cont-ave std Sw-ave std | <u>Signal Transduction</u> 0.004 1.05 0.32 2.48 | <u>Transcription Factor</u> 0.037 0.94 0.10 2.14 |

9 ...

APPENDIX C

| Name/Description Brain creatine kinase B: The creatine brain kinase B (CKB) enzyme is proposed to have a pivotal role in the | regeneration of ATP in the Process system. Intestinal alkaline phosphatase (IAP); intestine, (kidney) a membrane-bound metalloenzyme catalysing cleavage of inorganic phosphate nonspecifically from a | wide variety of phosphate esters. Eosinophil peroxidase; is one of the blood (eosinophils) granule enzymes in the eosinophil- specific granules and is distinct from | myeloperoxidase. Erythropoietin; The glycoprotein produced in the kidney or hormone erythropoietin regulates the liver of adult and the liver hormone erythropoietin regulates the liver of oxygen in the blood by of fetal or neonatal modulating the number of circulating mammals | erythrocytes. Insulin receptor (IR) Telomeric protein mTRF1; a telomere ubiquitous repeat binding factor packages the long tandem arrays of the double- | mammalain telomeres. Fos B; a nuclear protein of 338 ubiquitous amino acids presenting a 70% homology with c-fos, whose expression is activated during GO/G1 transition. Similar to c-fos, fos B protein plays a role in control of gene |
|--|--|--|---|---|---|
| GenBank X04591 | M61705 | D78353 | M12930 | J05149 U65586 | X14897 |
| std 18.89 | 1.34 | 8.36 | 1.50 | 2.34 | 20.11 |
| SW-ave ,40.81 | 4.52 | 15.52 | 0.66 6.74 | 9.80 | 34.54 |
| e std 4.87 | 0.94 | 0.01 | 0.66 | 0.01 | 0.01 |
| std Cont-ave std 9.71 5.11 4.87 | 1.09 | 0.01 | 1.18 0.77 | 0.29 0.15 0.00 0.00 | 0.00 0.01 |
| std 9.71 | 1.77 | 0.00 0.01 | 1.18 | 0.29 | 0.00 |
| Low-Low-Hi p value CR-ave std Cont-ave std 0.013 5.61 9.71 5.11 4.87 | 0.013 1.48 1.77 1.09 | 0.00 | 1.12 | 0.00 | 0.016 0.00 |
| Low-Low-Hi p value CR-av 0.013 5.61 | 0.013 | 0.015 | 0.001 | 0.009 | 0.016 |

-1117-

| Name/Description Retinoid X receptor-gamma (mRXR-ubiquitous (one isoform in Retinoid X receptor-gamma (mRXR-ubiquitous (one isoform in gamma); a kind of nuclear receptors adrentals, kidney, and of retinoids which play a liver; another in brain and fundamental role in regulating normal lungs; both are expressed cell proliferation and differentiation. strongly in heart and The retinoid X receptors (RXRs) muscle) | transcriptionally active heterodimeric RAR(the retinoic acid receptors)/RXR or homodimeric RXR/RXR complexes on DNA. Evx1 protein; A murine even-skipped embryos (eve) homologue. During embryogenesis, Evx 1 shows a biphasic expression pattern. The early and late transcription pattern is completele with a role of Evx 1 in experiment to bosterior. | information along the embryonic axis information along the embryonic axis and in specifying neuronal cell fates within the differentiating neural tube. Wnt-11 protein; The Wnt gene family embryos Wnt-11 protein; The Wnt gene family embryos molecules a set of signalling arteriosus, somites at the molecules, thought to play an medial junction of the important role in key processes of dermatome and the embryonic development, WNT11 has myotome, and limb bud | possible roles in the development of mesenchyme) skeleton, kidney and lung. Tsx; a gene of unknown function tetis that was shown to be expressed specifically in the testis. It locates 3' form the Xist gene which involves in the X inactivation. |
|---|---|--|--|
| GenBank X66225 | X54239 | X70800 | 96766X |
| 1.12 | 9.38 | 24.84 | 3.06 |
| SW-ave std 3.62 1.12 | 16.67 | 55.35 | 4.73 |
| • | 1.63 | 0.00 | 0.57 |
| std Cont-ave std 0.98 0.66 0.56 | 1.84 | 0.00 0.00 | 0.18 0.44 |
| std 0.98 | 3.18 1.84 | 0.00 | |
| w-Hi CR-ave 0.98 | 2.31 | 0.00 | 0.039 1.10 |
| Low-Low-Hi p value CR-ave std 0.005 0.98 0.98 | 0.023 | 0.006 0.00 | 0.039 |

<u>-</u>

| Name/Description Rds protein/peripherin; a eye? photoreceptor disc membrane- associated glycoprotein involved in retinal degeneration slow. It is 92.5% identical to the sequence of the bovine photoreceptor-cell protein peripherin. It may function as an adhesion molecule for stabilization of the outer segment discs. Hepatitis virus MHV-A59 defective? interfering (DI) RNA; RNA of defective-interfering virus formed earlier in infection, can mediate homologous interference. |
|--|
| GenBank X14770 |
| 2.39 > |
| SW-av 15.23 |
| 0.02 0.02 0.59 |
| Low-Low-Hi p value CR-ave std Cont-ave std 0.043 0.00 0.00 0.01 0.02 0.02 0.043 0.09 1.04 0.68 0.59 |
| o.00 1.04 |
| CR-ave 0.00 0.99 |
| Low-Low-Hi p value CR-0.043 0.00 |

APPENDIX D

| | | in lung, and t, stomach, t not in brain | ssed in the is, but barely the liver and le | strongly by in lyntphoid ietic tissues |
|---------------------------------|---|---|--|--|
| Name/Description tissue | SOX11; Sox genes, which encode ubiquitous transcription factors related by a DNA-binding motif termed the HMG box, are known to have diverse roles in vertebrate differentiation and development. SOX11 was suggested a role in neuronal maturation and an additional role in tissue modelling during | development: surfactant protein D (Sftp4); Surfactant predominantly in lung, and protein-D (SP-D) is a collectin found also in heart, stomach, protein-D (SP-D) is a collectin found also in heart, stomach, associated with surfactant in the lung, and kidney but not in brain associated with surfactant in the lung. | characterized as an opposite the control of the cytosolic constant and a chemoattractant incroorganisms and a chemoattractant for phagocytic calls and a chemoattractant from the phosphatidylinositol and to the fiver and phosphatidylinositol and the fiver and the fiver and kinase (PIAPEK) have been identified as skeletal muscle one of the cytosolic components | required for ATP-dependent, Ca2+· activated secretion. Sialoadhesin; Sialoadhesin is a expressed strongly by Sialoadhesin; Sialoadhesin is a expressed strongly by macrophage-restricted adhesion macrophages in lyniphoid molecule of 185 kDa that mediates sialic and haernopoietic tissues acid-dependent binding to cells. |
| | 0.07 AF009414 | 0.23 L40156 | 0.29 D86176 | 0.07 236293 |
| std | 0.07 | 0.23 | 0.29 | 0.07 |
| CONT- std Swiched- std GenBank | ave 0.04 | 0.38 | 0.54 | 0.27 0.61 |
| std | ave 0.30° 0.04 | 0.25 0.38 | 0.17 | 0.27 |
| CONT- | ave 0.20 1.17 | 0.43 1.21 | 0.10 1.26 0.17 0.54 | 0.33 1.31 |
| std | 0.20 | 0.43 | 0.10 | 0.33 |
| Hi-Hi-Low p value CR-ave std | 1.42 | 1.01 | 0.013 1.02 | 0.032 1.16 |
| Hi-Hi-Low | . 0 | 0.041 1.01 | 0.013 | 0.032 |

APPENDIX E

| Hi-Low-Low p value C | S ch | std | CONT- | std | CONT- std Switched-ave std | std | GenBank | Name/Description . Tissue |
|-------------------------|-------|------------|-----------|-------------|----------------------------|------|----------|---|
| 0.001 | 3.65 | 0.92 | 0.32 | 0.10 • 1.10 | 1.10 | 0.33 | D83262 | Neuronal glutamate transporter EAA14: Brain (neurons) induces high-affinity uptake of L-glutamate |
| 4100 | 2.73 | 0.31 | | 1.09 | 0.42 | 0.52 | X90778 | Histone H2B Combrane Aratein 1 eve? |
| 0.017 | 2.25 | | 0.79 | 0.74 | | 0.50 | M96760 | rod outer segment menbrane process (90m-1): Rom-1 and peripherin are related |
| | | | | | | | | retina-specific integral membrane protein localized to the photoreceptor disk rim, where they may act jointly in the photoreceptor disk |
| 0.018 | 7.93 | 4.23 | 4.23 0.00 | 0.00 1.16 | 1.16 | 1.25 | X14971 | biogenesis. alpha-adaptins are components brain and liver alpha-adaptin (A): Adaptins are components which link clathrin of the adaptor complexes which link clathrin |
| | | | | | | | | to receptors in coated vesicles. The alpha- adaptins, which are found exclusively in |
| 6 | | 76 1 36 1 | c | 0 | 00.00 | 0.00 | D49429 | endocytic coated vesicles PW29: calcium binding protein with strongly |
| 0.02 | 9 | ř | 8 | | | | | oligoproline motif, a mouse nomidiog of expression motifications. Medipolicy, has been implicated festis. Urain, bidney and heart |
| 0.022 | 10.70 | 10.70 6.08 | 0.00 | 0.00 1.38 | 1.38 | 1.61 | M55617 | functioning in sister chromatid cortesion. mast cell protease-4: a socretory granule connective tissue serine protease of the peritoneal connective |
| 0.023 | 1.78 | 1.78 0.51 | 0.84 | 0.63 | 0.21 | 0.31 | AF013253 | tissue mast cells (CTMC). preprocortistatin (Cort): Cortistatin is a 14-brain (cerebr. preprocortistative neuropeptide with strong cortex and |
| | | | | | | | | structural similarity to somatostatin and is hippocampusl expressed predominantly in cortical GABAergic interneurons. Administration of |
| | | | | | | | | cortistatin into the brain ventricles specifically enhances slow-wave sleep, presumably by antagonizing the effects of acetylcholine on cortical excitability. |

| HI-Low-Low | cR- | std | CONT | std | CONT. std Switched-ave std | std | GenBank | Name/Description Tissue |
|---|-------------|------------------|--------------------------|-----------|----------------------------|-------|---------|--|
| 0.032 | ave 2.12 | | ave 0.73 | 0.61 0.37 | 0.37 | 0.39 | U02982 | secretogranin III (SgIII): an acidic brain- and chromogranin/secretogranin-like protein of pituitary-specific unknown function that is present in the storage vesicles of many neuroendocrine |
| 0.033 | 1.70 | 0.28 | 1.70 0.28 0.70 0.52 0.54 | 0.52 | 0.54 | 0.45 | U39818 | cells. tuberin (TSC2): the tuberous scierosis 2 ubiquitous (TSC2) gene product, which contains an activity that specifically stimulates the contains of the section of the |
| 0.037 | 21.18 | 21.18 14.98 0.00 | 0.00 | 0.00 0.00 | 0.00 | 0.00 | 017407 | intrinsic of factory of the state of the sta |
| 0.038 16.26 11.58 0.00 | 16.2 | 6 11.58 | 0000 | 00.0 | · 00:0 | 00:00 | X72862 | factor; an endogenous imprinted gene on the proximal region of chromosome 11. This gene is transcribed exclusively from the unmethylated paternal allele, whilo the methylated maternal allele is silent. Beta-3-adrenergic receptor; a member of the mainly expressed super-family of G protein-coupled receptors; in mouse brown plays a role in the control of cAMP and white accumulation and may be involved in the adipose tissues control of energy expenditure in fat tissue. |
| <u>Transcrioption Factor</u> 0.007 2.57 0.46 | 2.57 | 100 Factor | 0.70 | | 0.71 0.41 | 0.52 | L10409 | Fork head related protein (HNF-3 beta): in Adult liver. addition to its known functions as embyonic node, transcriptional activators in adult liver, play a notochord, floor role in body axis formation, neural tube plate and gut patterning and definitive endoderm formation during gastrulation. |

| Tissue Name/Description | Transcription factor FKH-2: a member of the Expressed in winged helix or "forkhead" transcription embryos and factor family; expression patterns of the fkh- becomes or the fkh-becomes and HNF-3 beta, are overlapping in restricted to the | midbrain early stages of gestation. Heat shock transcripton factor 2; binds to the Ubiquitous heat shock element (HSE). | Zinc finger protein (kid-1); a putative renal Noticy and cycles transcription factor; regulation during | ontogeny and in response to the specifically toxic injury Fkh-5 (also known as Mf3 and TWH); a Specifically member of the 'winged helix' or 'forkhead' expressed in the transcription factor gene family central nervous | SWI/SNF complex 60 KDa subunit (BAF60a); Ubiquitous mammalian homologue of yeast SWI/SNF complex, also referred to as BRG1-associated to Application of | tactors (DATS), required to the composing transcriptional activators by opposing chromatin-dependent repression of devicement and (in mamals) is likely transcription, and (in mamals) is likely dedicated to developmentally distinct functions. NFIL3/E4BP4 transcription factor; nuclear Blood factor regulated by IL-3/adenovirus E4 promoter binding protein in a distinct growth factor-regulated signaling pathway that is responsible for the survival of early B-cell progenitors | |
|-------------------------|--|--|---|---|---|---|-------------------|
| GenBank Nam | X86368 Tran "win factor | early K61754 Hear | L77247 Zinc tran | onto toxi X92592 Fkh. mer tran | U66620 SW mar | trac trar chri trar ded ded fun fun pro fac fac fac fac | |
| | 87 | 1.39 X | 0.77 L | oo | 00.0 | 0.17 | |
| Switched-ave std | 6.27 | 0.80 | 1.05 | 00.0 | 0.22 0.00 | . 0.22 | |
| ţ | 0.00 | 0.00 | 0.00 | 0.00 | 0.22 | 0.26 | |
| ; | CK- std CON ave ave 36.94 12.40 0.00 | 12.24 3.07 0.00 | 4.43 0.96 0.00 | 16.08 10.27 0.00 | 36.92 17.87 0.13 | 1.95 0.59 0.87 | Cell Growth/Cycle |
| 3 | p value 0.007 | 0 | 0.001 | 0.024 | 0.007 | 0.005 | Cell Gro |

| HI-Low-Low | | std | CONT- | std | CONT- std Switched-ave std | std | GenBank | Name/Description |
|-------------------|--|------------|--------------------------|----------------|----------------------------|-------|--------------|---|
| . 0 | 8 | 3.83 | 9.00 0.00 | 0.00 0.00 | 0.00 | 0.00 | L25602 | Bone morphogenatic protein 2 (BMP-2); Ubiquitous pleiotropic functions range from extraskeletal |
| 0.004 | 2.97 | 0.78 | 2.97 0.78 0.34 0.60 0.33 | 0.60 | 0.33 | 0.58 | 089080 | generation and regeneration; structurally related to transforming growth facto-beta s. activins, and inhibins Fibroblast growth factor 10 (FGF10): has expressed important roles in mediating mesenchymal-relatively epithelial cell interactions during abundantly in embryogenesis. In particular, Fgf10 is embryos and the predicted to function as a regulator of brain, lung, and at predicted to the development, prostatic growth much lower |
| 0.002 | 0.002 14.09 4.67 1.12 | 4.67 | | 1.93 0.00 | 00.00 | 0.00 | M30903 | and development and so on. heart heart B lymphocyte kinase (blk); a Src family Blood (specifically tyrosine kinase specific to B lymphoid cells expressed in the |
| 0.007 | 4.14 | 1.40 | 4.14 1.40 0.00 0.00 1.09 | 0.00 | 1.09 | 1.14 | X59398 | Tyrosine kinase receptor of the various adult PDGFR/CSF1R family (FIt-3); involved in tissues including development and function of various cell gonads and brain. |
| 0.008 | 1.64 | 0.34 | 1.64 0.34 0.00 | 0.00 | 0.71 | 0.62 | U22399 | lineages; unidentified ligand in placents, and ponads and hematopoietic and nervous hematopoietic systems. Cdk-inhibitor p57KIP2 (KIP2); a potent, tight- High levricomplaxes; and is suggested to be involved skeletal muscle, in decisions to exit the cell cycle during brain, heart development and differentiation. |
| Extracel 0.023 | Extracellular Matrix 0.023 24.61 5.47 | ix 5.47 | 00.00 | 0.00 0.00 7.30 | 7.30 | 12.64 | 12.64 M32136 | alpha-1 type IX collagen (COL9A1): a ubiquitous structural component of the extracellular matrix of connective tissues |

| Hi-Low-Low | ow CB- | std | CONT. | std | CONT. std Switched-ave std | std | GenBank | Name/Description Tissue |
|--|---------------|------|--------------------------|------|----------------------------|------|---------|---|
| 0.035 | 2.93 | 1.06 | 2.93 1.06 0.64 1.10 0.81 | 1.10 | | 0.21 | U43541 | s-laminin (also called laminin beta 2): a muscle homotogue of the B1 (beta 1) chain of the widely distributed basal lamina (BL) glycoprotein, laminin. It may affect postsynaptic differentiation. |
| DNA respeir 0.039 14.29 8.65 0.00 0.00 2.67 | pair 14.29 | 8.65 | 0.00 | 0.00 | 2.67 | 3.79 | 126320 | FLap endonuclease-1 (FEN-1): an enzyme Ubiquitous which functions in double-strand break repair flap resolution; it specifically cleaves DNA flap strands that terminate with a 5' single-stranded end; in addition to endonuclease activity, FEN-1 has a 5'-3' exonuclease activity, which is specific for double-stranded |
| | | | | | | | | |

APPENDIX F

| CR. CR. Cont. Cont. Std. ave std. aver aver aver aver aver aver aver aver | GenBank Name/Description L11333 Mouse carboxyssterase; serine- Predominantly in male livers dependent enzymes M74149 Creatine kinase B; plays an important liver, brain, skeletal niuscle, role in buffering ATP and ADP levels heart, intestines in tissues which have intermittently high and fluctuating energy demands and fluctuating energy demands of the complement 4b-binding protein (C4b- Liver binding protein); an abundant controls the activation of the complement cascade through the caption of the complement cascade through the complement cascade through the complement and the complement of the Liver, brain, skeletal muscle, of basic helix-loop-helix leucine zipper testis (bHLH-ZIP) transcription factors. D70849 Zic3; encodes a zinc finger protein, is Restricted in the cerebellum at expressed in the developing or the adult stage. matured central nervous system in a highly restricted manner. It's the vertebrate homologue of Drosophila odd-paired, which may play an essential role in parassgmental subdivision and in visceral mesoderm development. D37837 65-kDa macrophage cytosolic Hemopoitetic cells protein; is phosphorylated specifically in LPS-stimulated munine macrophages. a murine homologue of human L-plastin, recently identified as a novel transformation-induced |
|---|--|
|---|--|

| | and and | . <u> </u> | = |
|--|--|--|---|
| | ه ري ه | steri n, th | 0.0g |
| Cont. Cont. SW. GenBank Name/Description | std 0.35 U04268 Mouse stem cell antigen Sca-2 Early thymic precursor and precursor; a member of the Ly-6 mature peripheral B cells (not family, a group of small cysteine-rich mature thymocytes and cell surface proteins that are peripheral T cells) anchored in the membrane by a | glycosyl-phosphatidylinositol moiety. 9.018 0.51 0.05 1.20 0.24 1.37 0.40 D38580 Vomeronasal secretory protein I Specifically expressed in posterior (VNSP I); secretory protein, member of vomeronasal and posterior tynsp II); secretory protein, member of vomeronasal septurn, the the lipocalin superfamily ducts of which open into the | lumen of the vomeronasal organion 2, the predominant nuclear Testis-specific proteins of mammalian spermatozoa, is regulated during germ cell development |
| k Nan | n Mou fam cell anc | t S S | 1 Pro pro is dev |
| GenBan | U04268 | 038580 | M2750 |
| SW. | std 0.35 | 0.40 | 0.67 |
| sw. | ave 1.39 | 1.37 | 1.48 |
| Cont- | 8td ave 0.51 1.39 | 0.24 | 0.07 |
| Cont- | 1.55 | 1.20 | 1.03 |
| ç. | std 0.13 | 0.05 | 0.08 |
| క్ర | ave std 0.27 0.13 | 0.51 | 0.27 |
| ow-Fil-Fil value CR- CR- | 10: | .018 | 0.024 |

APPENDIX G

208 known genes: 2-fold or greater in CR vs. Cont at old and young age GenBank

| Transcription Factory Y00850 | Transcription Factor / Nuclear Notable / (Zfp2); Mkr-2; differentiation Y00850 Zinc finger protein 2 (Zfp2); Mkr-2; differentiation | Brain (Central and peripheral neurons) |
|------------------------------|---|---|
| | and/or maintenance of neurons | Developing CNS |
| x63963 | Paired box protein (Pax-6); transcription factor | Developing company. Mood: hone marrow cells; natural |
| X06762 | Homeo box B7 (Hoxb7); transcription factor; | beveloping amorpo, cross, construction with the second construction of the |
| | embryonic development; naemacrintion factor | Embryogenesis |
| X74040 | Homeo box A3 (noxas), water transcription factor; | Embryogenesis |
| X59251 | Homeo box instruke i wox.;; series in embryo | poo alosimo reibrea lescindo Esta de anos |
| 267747 | Zinc finger protein 62 (Zfp62); a member of a | Embryonic development and Skeretal, calcust models and sheep in adult |
| | multigene family encoding Zn mediated nucleic acid | |
| | binding proteins | Embryonic development, testes in adult |
| M36516 | Zinc finger protein 28 (41p.26); a member of a multigene family encoding 2n mediated nucleic acid | |
| | binding proteins | and the state during muscle differentiation |
| 1148721 | Zinc finger protein 60 (Zfp60); a member of a | Expressed transferring during massic commensus |
| | multigene family encoding Zn mediated nucleic acid | |
| | binding proteins; Kruppel associated boxes; | |
| | associated with transcriptional control | |
| X04435 | Glucocorticoid receptor 1 (Grl1); energy balance; | LIVER |
| | substrate uptake; liver | |
| X74134 | Nuclear receptor subfamily 2, group F member | רואפו |
| | (Nr2f1); COUP-TF1; orphan steroid hormone receptor; | |
| | transcription factor | |
| 000925 | Transcription elongation factor A 1(Tcea1); | Liver |
| | transcription elongation factor | |
| Y89264 | Zinc finger protein 37 (Zfp37); putative transcription | Liver |
| | factor; peroxisome proliferator responsive | liver and heart (embronic) |
| X56182 | Myogen factor 5 (Myf5); transcription factor | |

| 208 known genes: | 208 known genes: 2-fold or greater in CR vs. Cont at old and young age | Location |
|------------------|--|---|
| GenBank | Description | Liver tunn kidney |
| X76653 | Nuclear receptor subfamily 2, group F member 2 (Nr2f2); apolipoprotein regulatory protein 1; member | רוֹעפּוֹ, ומוּשׁ, ייִפּייִי לּי |
| | of the COUP-family of steroid hormone orpinan | |
| 1 24118 | Tumor necrosis factor induced protein 2 (Tnfip2): | Liver; monocytes |
| | putative transcription factor | Lymphocytes |
| U36575 | Nuclear factor of activated T cells, cytoplasmic 2 | Lymphocytes |
| 1140463 | Timor necrosis factor Induced protein 3 (Tnfip3); | Lymphocytes |
| 0.13463 | putative helix-loop-helix transcription factor activated | |
| | in T-cell acute lymphoblastic tenering | Lymphocytes |
| U19463 | Tumor negrosis ractor induced processing processing putative helix-loop-helix transcription factor activated | |
| | in T-cell scute lymphoblastic leukeillid | Many cell-types during development |
| ET61028 | Sine oculis-related homeobox 1 iloliiologac | |
| | (Drosophila) (3/X 1), Aneco | Many nonneuronal cells and tissues |
| 013878 | factor: represses expression of neuronal genes; | suppopulation and embroyonic: central nervous |
| Y12293 | Forkhead box F2 (Foxf2); transcription factor; a | Mesodermai itssues and composition system, eye, ear, and limb bud |
| | Homes hox D1 (Hoxd1); transcription factor; | Neurogenesis |
| X60034 | neurogenesis | Silvering properties (cells) |
| ET63177 | Pax-4 (Pax4); a paired-box transcription factor that | Pancreatic islet endocting progenition comp |
| | pays an important cells; role in endocrine cell pancreatic beta/delta cells; | |
| | development | Tools |
| M81077 | T-cell acute lymphocytic leukemia 2 (1812); putative | |
| | T-cell acute lymphoblastic leukemia | Spermatocytes. |
| X72697 | Meiosis-specific XMR (Xmr); transcriptional activator | Testis; lymphoid cell lineages, riccis; or specification, and later |
| | function? | becomes concentrated in the XY nuclear subregion. |
| | rate sessivition factor 1 (E4f1); DNA binding | Ubiquitous |
| X76858 | transcription factor | |
| | (I dilacipilati recie | |

| 208 known genes: | : 2-fold or greater in CR vs. Cont at old and young age Description | Location |
|-------------------------------------|---|--|
| X15842 | member of the lab family of | Übiquitous |
| X60136 | ion factor 1 (Sp1); transcription some hepatic glucose response | Ubiquitous |
| X80508 | ciated protein, 65 kDa (Yap); transcription | Ubiquitous |
| ET61461 | G-protein coupled receptor; poorly characterized | Unknown |
| Translation / Splic Y08260 | Ing / KNA Processing Factors Cytoplasmic polyadenylation element binding protein (Cpeb); RNA binding protein that promotes | Ubiquitous |
| X91656 | 3); splicing amily of SR alternative | Ubiquitous |
| U28419 | tion initiation factor eif-4C homologue | Ubiquitous |
| <i>Signal Transductio</i> L28756 | Gonadotropin releasing hormone receptor (Gnrhr); G- | Brain (anterior pituitar), reproductive organs |
| 231663 | onine | Brain (cerebral cortex, olfactory tubercle, and hippocampus) |
| X66118 L41495 | ate receptor, ionotropic, kainate 1 (Grik1) integration site (Pim2); serine/threonine kinase proliferation; mitogen stimulated; long-term | Brain (CNS), Immune and epithelial cells |
| 272000 | Btg3); negative control of | Brain, fibroblast |

| 208 known gene | 208 known genes: 2-fold or greater in CR vs. Cont at old and young age | Location |
|-------------------|--|---|
| GenBank | - | Brain, testes and spleen |
| X79082 | member of receptor tyrosine kinase family | Brain uterus, prostate gland, pancreas and kidney |
| 227088 | modeling of | |
| X58287 | tyrosine phosphatese, receptor-type, M | Capillaries in developing neural (issue, lung) |
| ET61628 | ubunit, prowth, | Liver |
| V00829 | mily r of and | Liver |
| 222821 | extracellular matrix glycoproteins and proteinases; Rab23; Ras-related small GTPase; protein trafficking; central regulatory elements of the intracellular transport machinery; regulate vesicle docking and | Liver |
| M25513 | fusion, organelle dynamics Guanine nucleotide binding protein, alpha transducing | Liver and others |
| 00000 | 1 (Gnat1) Guanine nucleotide binding protein beta 4 (Gnb4) | liver, brain, blood cell |
| M63658 U38501 | Guarine nucleotide binding protein, alpha inhibiting 1 (Gnail) | Liver; cerebral cortex; pancreauc acrisi com, |
| 030743 | Wee1 homologue (S. pombe) (Wee1); inhibits entry into mitosis by phosphorylation of the Cdc2 kinase | Lymphocytes Lymphocytes Lymphocytes Lymphocytes |
| ET61263 | Spleen protein kinase (Syk); signal transduction | |
| 248757 ET61665 | Intestinal tyrosine kinase; protein tyrosine kinase Discs-large tumor suppressor homologue (dlgh1); important role in the localization and function of | Mammary gland and intestine Neurons; epithelial cells |
| ET61399 | glutamate receptors and K(+) channels G protein alpha olfactory subunit; sensory | Olfactory epithelium |
| | transduction | Skeletal muscle |
| M14537 | Acetylcholline receptor 2022 | |

| 208 known genes: | 208 known genes: 2-fold or greater in CR vs. Cont at old and young age | Location |
|------------------|---|---|
| GenBank | Description Calpain 3 (Capp3); intracellular calcium-dependant | Skeletal muscle |
| X92543 | cysteine proteinase; tissue specific myofibrogenesis, | |
| 211574 | Son of sevenless 1, homologue 1 (Drosophila) (Sos1): | T cells |
| 211664 | Ras-specific exchange lector Son of sevenless 2 homologue 2 (Drosophila) (Sos2); | Tcells |
| U10440 | Ras-specific exchange factor Cyclin-dependent kinase inhibitor 1B (P27) (Cdkn1b); | Ubiquitous |
| 7764957 | MAP kinase kinase kinase (Map3k1); serine-threonine | Ubiquitous |
| E10123/ | kinase; regulates sequential protein phosphorylation pathways involving mitogen-activated protein kinases | |
| | (MAPKs) | Ubiquitous |
| \$45828 | NIMA-related expressed kinase (Nek I) | Thionitous |
| U65313 | Ras-GTPase-activating protein SH3-domain pinung | |
| ET62740 | Ankyrin 3 (Ank3); implicated in Na(+) channel | Wide distribution |
| | | |
| Hormone/Growth | Harmone/Growth Facotr/Cytokine/Chemokine | B cell properitors |
| X07962 | Interleukin 7 (IL-7); growth factor | of the least miscle and other |
| U66201 | Fibroblast growth factor homologous factor 1 (FGF-1); | Dialit, sheleter incoord are |
| U66204 | Fibroblast growth factor homologous factor 4 (FHF-4). | Brain (CNS) |
| | involved in nervous system development and involved dimeric | Endothelial cells, expressed in many tissues (including |
| X99572 | orotein member of the platelet-derived growth | liver) during embryonic development |
| | factor/vascular endothelial growth factor represented and morphogenic | |
| | activity on fibroblasts. | |
| 100424 | Interferon-beta | ia/ii |
| x07751 | Thyroid hormone receptors | Liver pointelial cells |
| ET62118 | Keratinocyte growth factor/fibroblast growth ractor-/ | רואכו |
| | precursor (ning) | • |

| 208 known genes | 208 known genes: 2-fold or greater in CR vs. Cont at old and young age | Location |
|-------------------|--|--|
| GenBank X57413 | Transforming growth factor-beta2 (TGFbeta2); cell | Liver stellate cells |
| ET62976 | Macrophage inflammatory protein receptor 1-alpha 2; Induces mobilization of intercellular calcium; beta- | Liver, brain, thymus, heart, spleen |
| VE2708 | Small inducible cytokine subfamily, member 2 (Scyb2) | Macrophages |
| 700428 | Lysozyme; signaling molecule for mast cells which | Macrophages, paneth cells (located in guodenal crypts) |
| ET61471 | Mast cell protease 7 (mMCP-7); mouse mast cell vuortee 2 released when mast cells are activated | Mast cells |
| J28404 | Macrophage inflammatory protein-1 alpha receptor; Macrophage inflammatory protein-1 alpha receptor; medians growth inhibitory affects of the chemokine | MIP-1aipha RL2 in liver and spleen |
| J58367 | Neuropeptide Y receptor Y5/Y6/Y2b (referred to as both Y5 and Y2b, has now been designated as Y6 in literature); (NPY-Y6); neuropeptide Y is an important regulator of nergy balance in mammals through its regulator existence and insulin secretage | Neurons, vascular smooth muscle cells |
| U10092 | Killer cell lectin-like receptor, subfamily A, member 6 (Kira6); Ly-49F; NK cell surface antigen; determinant of IL-2-activated NK cell specificity; inhibitory contract for interaction with MHC class I proteins | NK cells |
| M31419 | Interferon-activatable gene (204); mediates antimicrobial, immunomodulary and cell growth-regulatory activities of interferons; increased up to | Nucleoi |
| 704725 | Preproinsulin gene 1 | Pancreas and islets |
| X04724 | Preproinsulin gene II | Pancreas and islets |
| M92416 | Fibroblast growth factor (Fgf6); Fgf6 is the only known member of the FGF family whose expression is restricted to the muscle cell lineage during | Skeletal muscle |
| X58995 | Calmodiin-depandent protein kinase IV; | T cells |
| | munifunctional, sering times (1.00 2) | T cells |
| V00/b6 | Interierusi 2 receptor; cytokine receptor | Tcells |

| D13695 M28687 U49866 | Lymphocyte antigen 84 (Ly84); signal transduction protein 2 Alpha leukocyte interferon (MulFN-alpha A); inhibition of cell proliferation | T cells Ubiquitous |
|--------------------------------------|---|-----------------------|
| M28587 U49866 | Apha leukocyte interferon (MulFN-alpha A); inhibition of Jell proliferation | Ubiquitous |
| U49866 | | |
| | killer cell lectin-like receptor, subfamily A, member 3 (Kiras); interact with MHC class I (MHC-I) molecules on terrat cells | natural killer cell |
| | UI talgar cone | |
| DNA Replication / Repair / Applicate | Ref. 2. heter suppresses programmed cell death | Liver |
| 131532 | Cyclin G: auaments apoptosis; target gene of P53 | Liver |
| U25691 | Lymphocyte specific helicase; putative role in | T and B cells |
| L16435 | Tumor necrosis factor (ligand) superfamily, member 9 (Trifsf9),a member of the TNF family; proapoptosis | T cells |
| | facotor | Thioritous |
| E162746 | Brca 2 gene; familial breast cancer susceptibility gene; important in DNA double-strand break repair (DSBR) and DNA damage-induced cell-cycle checkpoint | |
| U04269 | Caspase 1 (Casp1); cysteine protease mediator of | Ubiquitous |
| | apoptosis | Thioritons |
| X58472 | KIN17, DNA-binding, nuclear protein, upregulated in response to UV and ionizing radiation; accumulated in the nucleus of protiferating fibroblasts; overexpression the nucleus of protein and chases. | |
| CT62470 | MIH1: DNA mismatch repair gene; function in | Ubiquitous |
| 6,473 | mutation avoidance; cell cycle checkpoint control; cytoxicity of various DNA-damaging agents; cytoxicity counted purified excision repair. | |
| ET61211 | transcription of the NA-dependent Elf-2 alpha kinase; double-stranded Ars) RNA-dependent protein kinase (PKR); key | Ubiquitous |
| | mediator of antiviral effects of interferon (IFN); active player in apoptosis | |

| OOR known genes: | 2-fold or greater in CR vs. | Location |
|-------------------|---|---|
| GenBank | | |
| X74351 | | Ubiquitous and adation leads to partial syndactyly of the limbs and |
| X71978 | Ft1, a novel gene felated to ubiquitin-conjugating enzyries, us thymic hyperplasia, suggesting impaired programmed cell death | Fr1, a novel gene felated to ubiquitin-conjugating enzymes, usicity in constant thymic hyperplasia, suggesting impaired programmed cell death |
| rensporter / Chan | ē | |
| Y09108 | | Brain |
| U14420 | gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3 (Gabrba); link binding of GABA (gamma-analysis binding of CABA (gamma-analysis binding of GABA) | Brain (CNS) |
| U48397 | Mercurial-insensitive water channel 1 (mMIWC1); allows water and small solutes to pass | Brain, eye, lung, kidney, heart, muscle Rvain Kidney |
| X97281 | K + channel beta-subunit, ion channel (Tro6); | Brain, kidney, heart and lung |
| ET61590 | Putative capacitative calculus chiry ordination of involved in calcium entry secondary to activation of receptors coupled by the Gg class of G protein. | Resin lung brain heart, intestine, kidney |
| X63100 | Gap junction membrane channel protein alpha / (Gja7); connexin45; gap junction protein; ion exchange channel | Brain. skin |
| ET63385 | Gap junction membrane channel protein beta o lopuo., connexin 30; forms transmembranous gap junction channels between adjacent cells | Brain: tissue distribution and protein poorly characterized |
| L42340 | Sodium channel 27 | Endothelium |
| ET61440 | Trp-related protein 3; cation chainer, essential capacitative agonist-activated capacitative Ca2+ entry; putative | |
| | Subunits of CCL charitors | Liver |
| M23383 | Syntaxin 3A, IER vesicular transport, membrane | Liver |
| 161670 | fusion | |

| Histone H10; Chromatin structure X16495 X16495 Histone H2A; Chromatin structure ET62908 Histone H3.2- (H3-D) and histone H4-D (H4-D); Ubiquitous Chromatin structure U62675 Histone H3.2-F (H3-F), histone H2a-1-F (H2a-F), Ubiquitous Histone H3.2-F (H3-F), histone H2a-1-F (H2a-F), Ubiquitous Wistone H2b-F (H2b-F); chromatin structure Biosynthesis and Metabolism UDP-glucuronosyltransferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution poorly X92122 Cerebroside and sulfatide biosynthesis; characterized | GenBank X83933 X83933 X80417 M30440 U03723 U49393 X84896 ET63248 U19521 U19521 | | Skeletal muscle Skeletal muscle Skeletal muscle, heart, kidney T cells; myelinating Schwann cells Ubiquitous Ubiquitous Ubiquitous Ubiquitous Ubiquitous Ubiquitous | cells |
|--|--|--|---|---------------------|
| H2A; chromatin structure H2B; chromatin structure H3.1-D (H3-D) and histone H4-D (H4-D); Ubiquitous In structure H3.2-616, and histone H2b-616; chromatin Ubiquitous H3.2-F (H3-F), histone H2a.1-F (H2a-F), Ubiquitous H2b-F (H3b-F); chromatin structure H2b-F (H2b-F); chromatin structure curonosyttransferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution curonosyttransferase 8 (Ugt8); key enzyme in Aracterized | | Histone H1b; chromatili structure | Ubiquitous | |
| H2B; chromatin structure H3.1-D (H3-D) and histone H4-D (H4-D); Ubiquitous n structure H3.2-616, and histone H2b-616; chromatin Ubiquitous H3.2-F (H3-F), histone H2a-1-F (H2a-F), Ubiquitous H3.2-F (H3-F); chromatin structure H2b-F (H2b-F); chromatin structure curonosyttransferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution curonosyttransferase 8 (Ugt8); characterized | | Histone H2A; chromatin structure | Uhiouitous | |
| H3.1-D (H3-D) and histone H2b-616; chromatin Ubiquitous H3.2-616, and histone H2b-616; chromatin Ubiquitous H3.2-F (H3-F), histone H2a.1-F (H2a-F), Ubiquitous H3.2-F (H3-F), chromatin structure H2b-F (H2b-F); chromatin structure curonosyttransferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution curonosyttransferase 8 (Ugt8); key enzyme in Grain (CNS and PNS); tissue distribution curonosyttransferase and sulfatide biosynthesis; characterized | | Histone H2B; chromatin structure | Uhiquitous | |
| H3.2-616, and histone H2b-616; chromatin Corporations H3.2-F (H3-F), histone H2a.1-F (H2a-F), Ubiquitous H2b-F (H2b-F); chromatin structure H2b-F (H2b-F); chromatin structure curonosyttransferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution curonosyttransferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution ide and sulfatide biosynthesis; characterized | J62672 | Histone H3.1-D (H3-D) and histone H4-D (H4-D), chromatin structure | Obtenitous | |
| H3.2-F (H3-F), histone H2a.1-F (H2a-F), Ubiquitous H2b-F (H2b-F); chromatin structure H2b-F (H2b-F); chromatin structure Gronosyttrensferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution curonosyttrensferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution defined and sulfatide biosynthesis; characterized | | Histone H3.2-616, and histone H2b-616; chromatin | Colduicoes | |
| 42b-F (H2b-F); chromatin structure 42b-F (H2b-F); chromatin structure curonosyltransferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution curonosyltransferase 8 (Ugt8); key enzyme in Arain (CNS) and PNS); tissue distribution curonosyltransferase 8 (Ugt8); key enzyme in Arain (CNS) and PNS); tissue distribution curonosyltransferase 8 (Ugt8); key enzyme in Arain (CNS) and PNS); tissue distribution curonosyltransferase 8 (Ugt8); key enzyme in Arain (CNS) and PNS); tissue distribution curonosyltransferase 8 (Ugt8); key enzyme in Arain (CNS) and PNS); tissue distribution | | structure Histone H3.2-F (H3-F), histone H2a.1-F (H2a-F), | Ubiquitous | |
| curonosyttransferase 8 (Ugt8); key enzyme in Brain (CNS and PNS); tissue distribution ide and sulfatide biosynthesis; characterized | | histone H2b-F (H2b-F); chromatin structure | | |
| curonosyltransierase o (Oglo), key characteristice and sulfatide biosynthesis; | sis and A | detabolism . Key enzyme in | and | tissue distribution |
| | | curonosyltransferase o (1919), relide | characterized | |

| 208 known genes: | 2-fold or greater in CR vs. | Location |
|-------------------|---|----------------------------|
| GenBank Y12257 | 1 | Brain (CNS) |
| D49438 | gamma-aminobutyrie acid (GABA) 25-hydroxyvitamin D3 24-hydroxylasa; metabolism | Kidney and intestine. |
| X07888 | and regulation of vitamin US 3-hydroxy-3-methylglutaryl coenzyme A reductase; 3-hydroxy-3-methylglutaryl coenzyme for cholesterol biosynthesis. | Liver |
| D21826 | Key regulatory continuous Cyridine monophospho-N-acetylneuraminic acid Cyridine monophospho-N-acetylneuraminic acid NeuGc) | Liver |
| U00932 | te transaminase nexosamine synthesi | Liver |
| L39373 | Mannoside acetyl glucosaminyl transferase 3 (Mgat3); transfers the bisecting GlcNAc to the core of complex, N-linked carbohydrates | Liver Liver |
| X72959 | ΙĔΙ | Liver and salivary glands |
| J04947 | Angiotensin converting enzyme (Ace); dipeptidyl carboxypeptidase that converts angiotensin I into the potent vasoconstrictor angiotensin II | Liver, Drain Thionirans |
| 109105 | Glucose phosphate isomerase (GPI); a housekeeping gene expressed in all tissues and organisms that utilize glycolysis and gluconeogenesis. | Objections |
| ET62525 | Polypeptide N-acetylgalactosaminyltransierase: 14 (polypeptide GalNAc transferase-14; ppGaNTase-14); fourth member of the mammalian UDP-GalNAc; Golgilike localization; 4 GalNAc-transferase controls the initiation of mucin-type O-linked protein glycosylation | Conquision (Sells) |
| X14489 | Thymidylate synthase (Tyms) | Ubiquitous (most cases) |
| *10.0: | Galactosidase, alpha (Gla); carbonyurate metacomini | |

Cellular Component (cell adhesion / membrane components / extracelluer matrix)

| 208 known genes: | 208 known genes: 2-fold or greater in CR vs. Cont at old and young age | Location |
|------------------|--|--|
| GenBank | Dascription | Brain (cerebral cortex in neonatal mice), thymocytes |
| ET62381 | K-cadherin/cadherin-6; present at external cell surrect at cell-cell contact sites; calcium-dependent cell | |
| | adhesion molecule (| Brain (CNS) |
| X95226 | Dystropleyin 10th, Communication mammalian neuromuscular junction | Brain (CNS) |
| X07215 | Proteolipid protein (Plp), main integral plotein of | |
| | myelin | Brain (CNS) |
| ET61336 | Cadherin 8 (Cdh8); adhesion molecule | Brain (subdivision of Barry Civ.) and spinal ganglia. Ild skeletal |
| X57377 | Myosin Va (Myo5a); cytoskeleton | myosin heavy chain gene expressed in fat-storing cells recommended in the collision heavy of the cells of regenerating liver |
| | 18-01-01-01-01-01-01-01-01-01-01-01-01-01- | Forthelial, endothelial, and mesenchymal cells in newborn |
| X66976 | Procollagen, type VIII, alpha 1 (Colda I); extracended | mouse tissue |
| | matrix: component of Dasai terrings and matrix: cardiac cardiac | lipocytes, of its cerist |
| M91602 | Myosin ilgili circii, cytoskeleton | regenerating liver; muscia |
| ET63188 | Fibroblast activation protein; cell-surface glycoprotein; | FIDIODIASIS |
| | member of the serine protesse railing, expressed the serine of tissue remodelling. | |
| M17376 | Alpha-1-acid glycoprotein I (AGP-1); membrane | Liver |
| | protein protein is a transmembrane protein | Liver |
| U49185 | Occludin (Ocin); occidum is a transmission of interact located at tight junctions and is known to interact | |
| | with other tight junction proteins | Liver |
| L02918 | Procollagen type V alpha 2 | Liver (epithelial cells) |
| 000830 | Epidermal keratin subunit; intermediate manage and protein; maintenance of epidermal cell shape and | |
| | resistance to mechanical trauma | Lymphocytes |
| X53176 | Integrin alpha 4 (Itga4); cell adhesion | Spleen, lung, testis, not reported in liver |
| X91043 | Erythrocyte protein band /.2 (cpu/.2), ccommon in Na + /K + permeability of cells | |
| 169136 | Cadherin 9 (Cdh9), calcium-binding membrane | Thymocytes |
| 3 | glycoprotein; cell adhesion molecule | Thymocytes |
| X97227 | CD53 antigen (Cd53); pairieunocyte construction | |
| | membrane glycopiotelli | |

| 208 known genes: | 208 known genes: 2-fold or greater in CR vs. Cont at old and young age | Location |
|--------------------|---|--|
| X75636 X75636 | Iduronato-2-sulfatase (Ids); degrades heparin sulfate and dermatan sulfate in lysosomas; deficiency causes fatal lysosomal storage disorder, mucopolysaccharidosis type II (the glycosaminoglycans heparin sulfate and dermatan sulfate accumulate); part of proteoglycans which bind, help package and store secretory molecules; function in cell adhesion and basal lamina formation | Ubiquitous |
| X66402 | Matrix metalloproteinase 3 (Mmp3); extracellular matrix-degrading metalloproteinase | Usidancus |
| U56734 | Mannose receptor, C type 2 (Mrc2); cell adhesion; antigen presentation | Wide tissue distribution |
| Call surface recep | | restrated and andothelial cells: lung (smooth muscle cells), |
| D78175 | | pointenal and encotings and heart (aortic smooth muscle colls) |
| M81000 | Signaling System, Gostrin releasing peptide receptor (Grpr); member of | Fibroblasts |
| | the G protein-coupled receptor mining | Late pre-B cells |
| M35684 ET61559 | Bradykinin B1 subtype receptor; G protein-coupled membrane bound; T-kininogen modulation during | Liver (ubiquitous) |
| M86441 | Fibroblast growth factor receptor 2 (Fgfr2); membrane-spanning tyrosing kinase; activated by | Liver parenchymal cells and others |
| U57612 | three members of the ror learning CD44 antigen (Cd44); receptor for hyaluronan; cell surface glycoprotein; hyaluronan clearance from the | liver, CNS, other |
| ET61693 | blood; lymphocyte homing and activation Leptin receptor (OB-R); transmembrane receptor | Liver, Lung, muscle, brain; developing bone, mesenchyme |

| Location | s, T cells, and monocytes | |
|--|---------------------------|----------------|
| 208 known genes: 2-fold or greater in CR vs. Cont at old and young age Description | Calcin Co | target tissues |
| 208 known genes: | ET62920 | |

| | Molecular Motors; | fraction beavy chain (mdhc1); axonemal | Brain, trachea, testis |
|--|-------------------|--|------------------------|
| | | Axonemal dynam leavy chair transcripty dynains are molecular motors that drive the beating of cilia and flagella; heavy chains are main components of multisubunit motor ATPase complexes called | |
| | | | Srain, trachea, testis |
| | | | Brain, trachea, testis |
| Nebulin; a family of giant myofibrillar proteins | | | Brain, trachea, testis |
| | | Nebulin; a family of giant myofibrillar proteins | |

Serum Protein/Secreted Protein

| 208 known genes: | 208 known genes: 2-fold of greater its on vs. com at the company of the company o | |
|-------------------|--|--|
| GenBank V00743 | Alpha fetoprotein (Afp); main component of mammalian fetal serum; synthesized by visceral endoderm of the yolk sac and by fetal liver; blood level decreases after birth; synthesis reactivated in liver tumors | Liver (fetal & adult) |
| Immune Cell Funct | | i |
| M88242 | prostaglandin-endoperoxide synthase 2 (Ptgs2); putative mediator of inflammation; induced by growth focus and cytokines | Fibrobiasts and monocytes |
| L38281 | Introduce and Systems gene 1(lrg1); activated by bacterial incomment | Macrophages |
| U43384 | Cytochrome b-245, beta polypeptide (Cybb); a flavocytochrome that mediates the transfer of electrons from NADPH to molecular oxygen in the | Phagocyte |
| V08028 | Immunity-associated protein, 38 kDa (Imap38) | Spleen |
| X16592 | Cytotoxic T lymphocyte-associated protein 2 beta (Ctla2b); homologue of cysteine protease proregion; | T cells |
| Others | | Alaha is expressed in most tissues; beta is expressed in |
| ET62336 | DNA ligase III-beta; DNA ligase III exists as two distinct isoforms denoted alpha and beta | testes and during spermatogenesis |
| X61449 | nucleosome assembly protein 1-like 1 | Brain; expression poury characterized |
| 128819 | Involucrin (IvI); a glycine-, serine- and cysteine-rich protein expressed late in differentiation of grandular | Chicarries |
| X99251 | Repetin (Rptn); calcium-binding; similar to intermediate filament-associated proteins profilaggrin | Epithelia of forestomach and tongue |
| | and trichohyalin; expression during late epidermal | |

| And Good | Description | רספמוסוו |
|-------------------|--|---|
| ET61424 | | Hematopoietic tissues |
| U73915 | Phosphate regulating neutral endopeptidases on the X chromosome (Phex); mineralization of Autroalitian matrix by osteoclasts | Kidney, bone |
| ET61364 | Meprin beta subunit isoform (Mep-1beta); meprins are membrane-bound oligomeric metalloendopeptidases, contain alpha and/or beta | Kidney, intestine, not reported in liver |
| 060330 | Proteaseome 3 (Psme3); Ki antigen; cell proliferation; enhances generation of class I binding | Liver, neurons, broad tissue distribution |
| X16490 | Plasminogen activator inhibitor , type II (Planh2); Plasminogen activator inhibitor, inactivates urokinase-type plasminogen activator and regulates degradation of the extracellular matrix; one form is cytoplasmic the | Liver; bone-marrow, spleen, lung, thyrnus, skin |
| X58169 | T-complex protein 10a (Tcp10a); Tcp-10 gene has T-complex protein 10a (Tcp10a); Tcp-10 gene has been established as a molecular candidate for the T complex responder locus which plays a central role in the transmission ratio distortion phenotype expressed by males heterozygous for a T haplotype. | Male germ line |
| 246299 | Sperm autoantigenic protein 17 (Sp17); sperm specific protein; calmodulin binding protein | Mammalian testis; sperm-specific |
| M26940 ET63259 | Casein beta (Csnb); milk protein Cea14 gene (carcinoembryonic antigen family members); unknown function; member of the | Many cea genes expressed in fetal liver |
| ET63260 | Cea15 gen (carcinoembryonic antigen family members); unknown function; member of the | Many cea genes expressed in fetal liver |

| GenBank ET63261 | | |
|--------------------|--|--|
| ET63261 | GenBank | in fetal liver |
| | Cea16 gene (carcinoembryonic antigen family members); unknown function; member of the | Many cea genes expressed in total many cea |
| M20567 | inmunoglobulin superfamily Heat shock protein, 70 kDa 2 (Hsp70-2); not induced by heat shock; developmentally regulated in | Meiotic phase of spermatogenesis |
| | ular hem | Muscle |
| X04405 | 5 | Nasal epithelium. |
| ET63205 ET63156 | Odorant binding protein 19 Disabled homolog 1 (Drosophila) (Dab1); adaptor | neuronal and hematopoietic cells |
| 00000 | Molecule in neural development | Olfactory and testicular cells |
| U96701 | Serine protease inhibitor 15 (Spi15); regulator of extracellular proteolysis | Predominantly in tests |
| ET63408 | Capping protein beta 3 subunit; a novel isoform of actin-binding protein; a component of the cytoskeletal calyx of the mammalian spern head. | Spermiogenesis |
| ET62832 | Perforatorial protein (PERF 15); a nover restrough protein; sequence similarities to a family of lipid binding proteins; major component of the rat sperm perinuclear theca. | Testis |
| 238118 | Synaptonemal complex protein 1 (Sycp1); pairing or chromosomes during meiosis | Tectis |
| M19413 | Tubulin alpha, related sequence 1 (1008-151) | Testis; synaptonemal complex protein 1 is also expressed |
| Y08485 | Synaptonemal complex protein a toyopol, per the lateral element of the synaptonemal complex; a meiosis-specific protein structure essential for meiosis-specific protein structure | in embryonic ovary, adult brain and testis |
| X96737 | Synapsis of normonagous chromosomes in Synapsiobrevin like 1 (Sybi1); housekeeping gene; X-linked; inactivated on one X in every female cell, | Ubiquítous |
| X92842 | Surfeit gene 6 (Surf6); involved in a nucleolar ribosome maturation; housekeeping | ubiquitous (nucleolus) |

| Location | Uncharacterized | Uncharacterized, probably neuronal | |
|----------|--|--|---|
| | GenBank WW domain binding protein 6; WW domain is a Uncharacterized ET62791 globular protein domain that is involved in mediating protein-protein interaction and that ultimately protein-protein interaction and that ultimately participates in various intracellular signaling events; www domain mediates protein interaction by | bin Neosin/lark; RNA-binding protein; Drosophila Uncharacterized, probably neuronal Neosin/lark; RNA-binding protein; Drosophila Uncharacterized, probably neuronal homologue encodes an element of the clock output | contracting adult eclosion (circadian rhythm) |

*** APPENDIX H

| 142 kno | wn genes | :: 2-fold u | 142 known genes: 2-fold up in young CR vs young Control and | |
|---------|-----------------------|------------------------------------|--|--|
| unchang | ed in old | unchanged in old CR vs old Control | d Control | |
| f-fest | t-test no t-test Bank | | notype * ation | |
| | | Bank | | |
| | | | | and positive liver and others) |
| 0.083 | 0.001 854 | 854 | | פונופוופו כפוים וויים פוים ביים |
| | | | oprotein 1; acts as a receptor for | |
| | | | ement membrane components | nt membrane components |
| 0.010 | 0.000 664 | | rin A5 (Efna5); Eph-related receptor 170 VI. | |
| | | | S; essential for proper axon guidance and | |
| | | | | |
| 0.084 | 0.014 122 | | assium inwardly-rectifying channel, rons | |
| - | | | family J, member 6 (Kcnjo); o proteint | |
| | | | vated; play a role in resting potential and | |
| | | | trolling excitability of the cell | the but not in thymus or pancreas |
| 0.425 | | 135 and | 0.008 135 and tin receptor (Lepr); Obr; leptin is a key r, upidutous, but many | יייין מיייין |
| : : | | 861 | ght control homone; mutation of the lepting | |
| | | | ptor causes obesity | in adult liver, CNS. |
| 0.346 | 0.008 701 | 701 | | (HDIII); nest in liver and hour committee; intestine |
| 5 | | | scriptional cell cycle repression; tumor literatu | חק כפווז, וכפון, וכיום, ייינים, ייינים אינים, ייינים אינים, ייינים, יי |
| | | | ÖN | ene |
| 0 117 | 0.0005603 | 5603 | aete-scute complex homolog-like elopin | |
| | | | sophila) (Asci1); helix-toop-helix protein nonly | |
| | | | scriptional factor; controls a basic | • |
| | | | ration in development of neuronal | |
| | | | enitors in distinct neural lineages | |
| 127 | | 0 0074120 | ivin receptor IIB (Acvr2b); receptor for ryo, testis | estis |
| 0.12 | |) | vins, which play an important part in | • |
| | | | oderm induction | |
| 0 374 | 1 | 0.006 546 | -ribosylation-like 4 (Arl4); ADP-pocyte | ADP-pocytes, upiquitous |
| 5 | | | sylation factor like protein 4; involved in | |
| | | | ation of transport vesicles; expressed iii | |
| | | | erentiating cells | |

| binding protein 1 (Aebp1); transcriptional eoblasts and adipose tissue essor with carboxylpeptidase activity; no scription during adipocyte differential or oblast calcification | aline phosphatase 3, intestine, not will stille, ficiney iring (Akp3); intestinal alkaline sphatase (IAP); a membrane-bound alloenzyme catalyzing cleavage of ganic phosphate nonspecifically from a evariety of phosphate esters. | and ylase 2, pancreatic (Amy2); J00361 creas, liver and many others se alpha-amylase-like gene; glycogen stion and mobilization | yloid beta (A4) precursor protein-binding, rous ily A, member 2 (Apba2); X11 protein e: X11 protein binds amyloid precursor ein; receptor trafficking; may regulate the essing of amyloid precursor protein to the loid beta peptide | lipoprotein CII (Apoc2); required for I liver, adult liver, intestine and peritoneal macrophages lysis of triglycerides by lipoprotein lipase | _ | ein deite (Csnd); epsilon-casein (milk mary giarius ein) ein) 8 antigen (Cd48); BCM-1; Blast-1; face of leukocytes | iates cell adhesion division cycle 25 homolog C (S.n spleen and thymus division cycle 25 homolog C (S.n spleen and thymus visiae) (Cdc25c); nine/tyrosine phosphatases that activato lin-dependent kinases; control of sitions between phases of cell division |
|--|--|--|--|---|-----------|--|--|
| 478 | 1705 | 361 an | 676 | 216 | 573 | 740 | 299 |
| 0.027 | 0.0271705 | 0.009 361 | 0.001 676 | 0.006 216 | 0.006 573 | 0.004 740 | 0.024 562 |
| 0.856 | 0.221 | 0.592 | 0.125 | 0.071 | 0.371 | 0.062 | 0.796 |

| protein ely expressed during development also in thymus ng protein | with during development | 200000000000000000000000000000000000000 | | | nest in pachytene spermatocytes, also in early | ryogenesis | SI | ryonic gonads and testicular germ cells | | | | ensin related sequence cryptdin peptide eth cells of the small intestine, smooth eth cells) (Defor-rs1); CRS1C; | | ryo, not in adult liver | | | | ryo and skin | | | - bloods (bionitons) | Opinate (unique of property) | | | - | | ONIA for E2E-5 protein | transcription factor 5 (E215); M. musculus minory to 1 | | oietin gene, complete cds | |
|---|-----------------------------------|--|--|---|--|------------|---|--|-------------------------------------|--|-------|--|-------------------|-------------------------|------------------------------|--|----------|-----------------------|--------------------------------|---|---------------------------------|---|---------|----------------------------------|-------------|-----------------------------------|------------------------|--|--|--|--|
| ular retinoic acid binding protein 6 bp.1); intracellular pipid binding protein | a high affinity for retinoic acid | omobox homolog 1 (Drosophila HP1 Bene; 44, Hurrous carring 41); Hamologous to Drosophila HP1 gene; | ifs chromatin, rendering heritable changes | gene expression; activates of singleses | is by (Caphy): remulator of transitions hest | | ochrome c, testis (Cyct); maintains tis | Throus spanial general general general general of the general control of the general g | polypeptide 4 (Ddx4); DNA helicase; | ortant role in determination events of | cells | ensin related sequence cryptdin peptide eth cells) (Defor-rs1); CRS1C; | microbial peptide | (Drosophila) (DII1); | communication regulating the | rmination of various cell fates during | elopment | 1 (Dsc1); a "skin-typ | mosomal cadherin; formation of | tinized epithelial structure during mouse | elopment; cell to cell adhesion | hanous homolog 1 (Drosophila) (Diap1); oblasts (uniquitoda) | cell mo | cytokinesis; Rho regulates actin | ng profilin | hanous homolog 1 beneath specific | ma membranes | transcription factor 5 (E215); M.musculus miny 191 E21 | like module containing, mucin-like, noming | broggietin (Eng): M12930 Mouse erythropoietin gene, complete cds | יייי ייייייייייייייייייייייייייייייייי |
| 715 | | 0.006 690 | | | 3 | 0.002 032 | 2 771 | 000 | 0.070 | | | 0.0343226 | | 1 903 | | | | 0.038 986 | | | | 0.002 963 | | | | | | 7 925 | 0.000 328 | 0000 | 0.010/2930 |
| 0.039 715 | | 0.006 | | | | 0.00 | 0.002 | 100 | 20.0 | | | 0.03 | | 0 031 | 3 | | | 0.03 | | | | | | î | | | | 0.027 | | | |
| 0.101 | | 0.051 | | | | 0.541 | 0.343 | 1 | 0.110 | | | 0.059 | | 2000 | ; ; | | | 0 167 | <u>;</u> | | | 0.475 | : | | | | | 0.174 | 0.899 | | 0.177 |

-147.

| | | | MRNA, 1122225 Mus musculus facionenital dysplasis (Fgd1) mRNA, |
|--------|-----------|-------------|--|
| 0.143 | 0.023 | 325 | ogenital dyspiasia nomolog (rgull, Ozesza mos mostala dyspiasia nomolog (rgull, Ozesza mostala dyspiasia nomolog (rgull, Ozesza mostala nomolog (rgull), Ozesza mostala |
| 0.993 | 0.0471737 | 1737 | specific gana 27 (Fsp27); M61737 M.musculus adipocyte-specific mRNA, partial cds |
| 0.062 | 0.046 535 | 535 | oblast growth factor 9 (Fgf9); U33535 Mus musculus ilbroblast growth factor 9 (Fgf9); |
| | | | plete cds |
| 0.993 | 0.003 853 | 853 | in 1 (Fbin 1); M: muscous (source witz 1) m: M: 90/(ibulin D form. |
| 0.358 | 0.006 854 | 854 | lin 1 (Fbin 1); M. musculus risonara vincaria (Fig. 2) |
| 0.150 | 0.002 | 660 | unction membrane channel protein pera 3 to 1900. |
| 0.341 | 0.000 953 | 953 | olin (Gsn); J04953 Mouse gelsolin gene, complete cos |
| 0.956 | 0.001 | 265 | osaminyl (N-acetyl) transferase 1, core 2 (Jouint), Crossos most acetyl transferase 1, core 2 (Jouint), Crossos most acetyl manyl, complete cds |
| 0.374 | 0.008 | 966 | th factor receptor bound protein 10 (Grb10); U18996 Mus musculus growin lactor leceptor bound |
| ; ; | | | ein (Grb10) gene, complete cds |
| 0.145 | 0.0410422 | 0422 | one 4 protein (Hist4);J00422 Mouse historie n4 gene, complete complete complete cds |
| 0.724 | 0.000 071 | 071 | eo box C5 (Hoxc5); U28071 Mus musculus nomedous de miseralus 3-rerosieroid reduciase |
| 0.207 | 0.037 519 | 519 | roxysteroid dehydrogenase-5, delta<5>-3-beta (nsususus), ivius musecus contractions and services of the servic |
| | | | USBS) mana, complete the state of the state |
| 0.116 | 0.003 973 | 973 | recon alpha family, gene 4 (finally), the control of the control o |
| 0.095 | 0.007 599 | 299 | rieron gamma receptor 2 (ing/z), occoso more more and a second mo |
| | | | r2) gene |
| 0.008 | 0.015 542 | 542 | rleukin 6 (116); |
| 0.566 | 0.008 359 | 359 | 359 mouse alpha-amylase-z gene |
| 0.086 | 0.009 761 | 761 | oncogene (Jun); Mouse mkNA for protein formorgades to minimize the protein alpha subunit |
| 0.785 | 0.046 | 0.046 08574 | voltage-gated channel, subfamily 3, 2 (noiszjiwas indocate promoter de la complete cds |
| | | | 3.21 Illing Complete Series 10 (Kr1.10): 100193 Mouse epidermal keratin type I intermediate |
| 0.128 | 0.018 193 | 193 | tin complex 1, acidic, gene 10 mm. |
| 0.053 | 0 026 313 | 313 | tin complex 1, acidic, gene 15 (Krt1-15); cytoskeletal structural protein D16313 Mouse cytokeratili |
| 3 | | | gene, complete cds |
| 0.071 | 0.002 889 | 688 | r cell lectin-like receptor, subfamily A, member 8 (Nrao), U12003 (Nras Industries of Translation) |
| | | | plete cds |
| 0.763 | 0.002 | 0.0024398 | rin (Lor); M34398 Mouse loricrin mKNA, complete cus |
| 0.088 | 0.016 503 | 503 | phoid enhancer binding factor 1 (Let 1); Diopos winds finances |
| 0.079 | 0.001 | 0.001 3099 | usculus epidymai sperm gene. |
| 0.701 | 0.026 | 0.026 3121 | usculus mRNA for alpha tectorin. |
| 0.016 | 0.019 | 0.019 3404 | usculus mRNA for axonemal dynain neavy criain traction in minimum. |
| 0.145 | 0.003 | 0.003 3397 | usculus mRNA for cytoplasmic oynem heavy chain the transmission in the control of |

| 0.000 3151 0.000 3151 0.000 3151 0.000 3431 0.000 3431 0.000 3431 0.000 3431 0.000 3431 0.000 3431 0.000 3431 0.000 323 0.000 3257 0.000 3257 0.000 3257 0.000 3257 0.000 3257 0.000 1628 0.000 3257 0.000 1628 0.000 1628 0.000 1628 0.000 3257 0.000 1628 0.000 1633 0.000 1647 0.000 1641 0.000 1641 | usculus mRNA for neural cell adhesion ecule. | (x2-3 gene. | usculus PR264 gene. | gen aptivated protein mRNA, complete cds | se DNA for neurotrophic factor, exon 3 and complete cos. | se DNA for vav-1, partial cds. | se mRNA for cytotoxic I-cell memorarie giycoproxii = 5 | se NLRR-2 mRNA for leucine-fichtebear process | musculus (Notcuz) miniar, compress | miscrifus ACF7 neural isoform 1 (mACF7) mRNA, partial cds. | musculus cea12 gene. | musculus cea9 gene. | musculus complement recepter (CRY) mRNA, partial cas Ispieeli specification musculus complement recepter (CRY) mRNA, partial cds. | musculus CRE-BP1 transcription tactor, novel spincer our, musculus CRE-BP1 transcription national mitochondrial | musculus glucose-6-phosphate denyarogenase (CO) 2/ 95000 | ein, exon o and partial cus. | musculus implantin mHNA, partial cus. | musculus laminin alpha ob chair territorial musculus laminin alpha ob chair control co | musculus mena protein tiwater time in the management of the manage | musculus microtubule-associated process | musculus P-glycollucian with a second | musculus polyreactive autoanticody, minoral and an artial cds. | musculus potassium chemical mix of mRNA, partial cds. | musculus puratree procession (TCRV-alpha-22.1) mRNA, variable region, partial cits. | musculus rearranged - comment of memory partial cds. | Musculus southin entire in Mana mana control de la control | musculus 1 cell redeptor a principal color and and another a menusculus 1 cell redeptor a principal color another a menusculus 1 cell redeptor a principal color another a menusculus 1 cell redeptor a principal color another a menusculus 1 cell redeptor a principal color another | musculus trp-felateu piverin 2 mary partial cds. | musculus tip-teated program of mineral in the program of the progr | Istoylated adulting their process | RCKS) mRNA, complete cds | plastic progression 1 (Npn1); M.musculus (Balurci 11 to annual) | |
|---|--|-------------|---------------------|--|--|--------------------------------|--|---|------------------------------------|--|----------------------|---------------------|---|---|--|------------------------------|---------------------------------------|--|--|---|--|--|---|---|--|--|--|--|--|-----------------------------------|--------------------------|---|--|
| | 3151 | 3209 | 3083 | 292 | 3431 | 3429 | 997 | 1015 | 210 | 27.50 | 3257 | 3255 | 1200 | 1528 | 2694 | | 1692 | 2692 | 2477 | 1218 | 1544 | 2236 | 1683 | 1621 | 1556 | 2586 | 2280 | 1439 | 1441 | 0474 | | 360 | |
| | 0.000 | 0.047 | 0.040 | 0.034 | 0.000 | 0.039 | 0.032 | 0.028 | 0.015 | 1000 | 000 | 0 028 | 0.034 | 0.000 | 0.043 | | 0.000 | 0.018 | 0.005 | 0.000 | 0.001 | 0.040 | 0.001 | 0.019 | 0.026 | 0.026 | 0.033 | 0.003 | 0.005 | 0.00 | | i | |

| 0.827 | 0.049 819 | 819 | ropeptide Y receptor Y1 (Npy1r); D63819 Mouse mRNA for neuropeptide Y-Y1 receptor, complete |
|--------------|------------|-----------|--|
| 0 186 | 0.000,0514 | 0514 | al (Nodal);X70514 M. musculus nodal gene, a TGF-beta-like gene |
| 0.133 | 0.046 163 | 163 | gin (Nog); |
| 0.238 | 0.029 033 | 033 | lear protein 220 (Np220); Mouse mRNA for nuclear protein, Nr 220, carripper con- |
| 0.062 | 0.000 804 | 804 | 804 Mus musculus zittingel process |
| 0.348 | 0.030 687 | 289 | nylethanolamina-N-methyltransferase (Pnint); L1200/ modes processer and place cds hyltransferase gene, complete cds |
| 0.307 | 0.005 | 279 | sphatidylinositol 3-kinase, catalytic, alpha polypeptide (Pik3ca); UO3Z/3 Mus musculus paidylinositol 3-kinase 110 kDa subunit mRNA, complete cds |
| 0.233 | 0.046 | 777 | spring of the special |
| 8070 | 0000 | 305 | ssium voltage gated channel, shaker related subfamily, member 1 (Kona1); Mouse MBK1 mRNA for |
| 3 | | | se brain potassium channel protein-1. |
| 0.958 | 0.038 789 | 789 | iferation-associated protein 1 (Plfap); M.musculus mkNA 101 ppc-204- |
| 0.063 | 0.000 | 594 | iferin related protein (PIff); Mouse mitted for prolifering and protein (1.11); Mouse mitted for prolifering for the protein (1.11); Mouse mitted for the prote |
| 0.146 | 0.009 532 | 532 | ein kinese C, beta (Pkcb); Mouse MKNA for protein kinase C ociani. |
| 60.10 | 0.009 | | ein Kinase C, eta (PKch); U90242 Mouse Inning In The Resident Company |
| 9.188 | 0.047 | 577 | ein kinase C, lamda (Pkc)); Mouse mknA for protein kinase C ramionogase name CAMP-dependent |
| 0.196 | 0.049 935 | 932 | ein kinase, cAMP dependent regulatory, type II alplia (rikarza), 302333 (moza |
| | | | ein kinase type II regulatury Subulin mitter, Commenter men for nerinuclear binding protein. |
| 0.542 | 0.011 720 | 720 | ein that interacts with C kinase I (Text) with a second in miner has a property of the complete |
| 0.374 | 0.013 768 | 168 | eoglycen 2, bone marrow (Frg2); L46/06 MUS Musculus mejor cario process. (m. 1 |
| 936 0 | 0.012 133 | 133 | analycan, secretory granule (Prg); Mouse mRNA for mastocytoma proteoglycan core protein, |
| . v. 30 | |) | lycin. |
| 0.904 | 0.022 239 | 239 | 58, member RAS oncogene family (Rab5b); X84239 M.musculus mrink for rabbb process |
| 0.010 | 0.027 | 247 | related C3 botulinum substrate 2 (Hac2); M.muscuns Environment ferror C large subunit |
| 0.115 | | 111 | |
| 0.463 | 0.023 642 | 642 | finger protein (C3HC4 type) 19 (Hnt 191A7 1942 Millusculus SCO 1914 MANA 3' end |
| 0.694 | 0.021 | 0.0275732 | inal vesicle protein 2 (Svp2); Mouse semantial vesicle secretary protein serim anyloid A exuns 3 |
| 0.714 | 0.032 | 0.0327790 | m amyloid A pseudogene (Saa-ps); M17/90 Mouse SAA4 gene chooling Scient Communication |
| | | | 4 Andrew Giebt 18 monein mana |
| 0.003 | | 280 | en in absentia 18 (Siah ID); M. musculus saint de professional (Scotty) 148687 Mus musculus voltage |
| 0.103 | 0.021 687 | 687 | ium channel, voltage-gated, type I, use purpopiede, to the lendant Na + channel beta-1 subunit gane, exons 4-6 |
| 0.328 | 0.002 | 268 | te carrier family 35 (CMP-sialic acid transporter), member 1 (Slc35a1); M. musculus miniva for con- |
| | | | ic acid transporter. |
| | | | 150 |

| ulated by retinoic acid gene 8 (Stra8); M.musculus mHNA for Stras protein. | interacting factor (Tgiff); X89749 M.musculus minks to introminent of the control | scription factor CP2 (1cfcp2); Mouse alpha-gloom transcription | 0.034 362 | West Stock in the second property of the second sec | of necrosis factor receptor superiority, member | frsf18); Mus musculus glucocorricola musculus | lly related protein precursor, mRNA, complete cas. | uitin-activating enzyme E1, Chr X (Ube Ix); ubiquitin-dependent protein deglacerion | 4170 | Oncogene (Vav); X64361 M.musculus vav mHNA | 0,048 01598 icular inhibitory amino acid transporter (Viaat); | entin (Vim); | A COMPLETE CONTRACTOR MANA COMPLETE COS | gless-related MMTV integration site 4 (Whitel); Woods words | 496 Murine H3.1 gene for histone H3.1 | figure profeso 30 (2/030): 2301 /4 M.domesticus (00/00/00/00/00/00/00/00/00/00/00/00/00/ |
|--|--|--|-----------|--|---|---|--|---|-----------|--|---|--------------|---|---|---------------------------------------|--|
| 0.114 0.037 287 | 0.043 0.007 749 | 0.394 0.002 6987 | 0.034 362 | 0.007 4625 | 0.004 534 | | | 0.306 0.013 581 | 0.006 859 | 0.005 361 | 0.048 01598 | 0.019 438 | 0.041 434 | 0.0019797 | 0.056 0.031 496 | 10000 |
| 0.114 | 0.043 | 0.394 | 0.177 | 0.402 | 0.533 | | | 9080 | 0.438 | 0.172 | 0.110 | 0.008 | 0.124 | 0.495 | 0.056 | |

APPENDIX I

| ue distribution | oblastic cells; or types of | s (these cells | uded oblasts, | tinocytes, | ocytes, kidney | nelial cells, and | or cells of | e, muscle, | , liver, kidney, | ach, colon, | state, and | ronal tissue) | | | | HINGOSINE 1. | RANSFERASE | .1.45) (UDP- | IDE | FERASE) | | FERASE) | Į | .ATED | E KINASE | EHK1 LIGAND) | ċ |
|---|--|----------------------------------|--|----------------|----------------|-------------------|-------------|-------------------|------------------|-------------|-------------------------------|----------------|---------------|-----------------|------------|-----------------------------------|---|----------------------------|------------------|---------------------|-------------|----------------------|-----------------|--|---|-------------------------------|-------------------|
| notype | .2. £. | e-derived extract s (these cells | ical to initiation of uded ation of cartilage oblasts, | its conversion | bone; is | cturally related | ransforming | wth facto-beta s, | vins, and | bins. BMP | aling is essential state, and | development of | letogenic and | rogenic cranial | ral crest. | 0.00.052 YDROXYACYLSPHINGOSINE 1- | A-GALACTOSYLTRANSFERASE | CURSOR (EC 2.4.1.45) (UDP- | LACTOSE-CERAMIDE | LACTOSYLTRANSFERASE | RAMIDE UDP. | LACTOSYLTRANSFERASE) | REBROSIDE SYNTH | 0.00 0.00 1.77.155HRIN-A3 (EPH-RELATED | EPTOR TYROSINE KINASE | AND 3) (LERK-3) (EHK1 LIGAND) | K1-L) (FRAGMENT). |
| unchaged in young CR vs. young Control ngCR ngCR ngCR ngCont ngCont st notype 16 17 18 19 20 21 | 0.00.374 | | | | | | | | | | | | | | | 0.00.052 | | | | | | | | 1.77.155 | | | |
| g Contro gCont r 20 | 0.00 | | | | | | | | | | | | | | | 0.62 | | | | | | | | 0.00 | | | |
| vs. youn JCont ng 19 | 0.00 | | | | | | | | | | | | | | | 1.08 | | | | ٠ | | | | 00.0 | | | |
| ung CR ng ngCR ng 18 | 29.61 | | | | | | | | | | | | | | | 1.49 | ? | | | | | | | 1.05 | | | |
| ed in yo | 0.00 | | | | | | | | | | | | | | | 1 43 | 2 | | | | | | | 2 96 | ì | | |
| nchage ngCR 1 | 0.00 | | | | | | | | | | | | | | | 28 |)) | | | | | | | 1 99 | | | |
| u and u | 0.003 | | | | | | | | | | | | | | | 0.021 | 20.5 | | | | | | | 0.016 | 2 | | |
| known genes: 2-fold up in old CR vs. old Control and unchaged in young CR vs. young Control R R ont ont ont st ngCR ngCR ngCR ngCont ngCont ng 1 2 3 7 8 9 16 17 18 19 20 | 8.75 11.48 3.04 0.00 0.00 0.00 0.003 0.00 0.00 29.61 | | | | | | | | | | | | | | | 2 | 3463 2.96 1.91 0.92 0.00 0.00 0.00 2.03 2.32 1.13 | | | | | | | 6 | 2773 1.04 0.96 1.92 0.16 0.00 0.00 0.00 1.00 1.00 | | |
| R vs. o | 00.0 | | | | | | | | | | | | | | | 0 | 0.0 | | | | | | | 0 | 5 | | |
| p in old Cl ont 3 | 0.00 | | | | | | | | | | | | | | | 0 | 5 | | | | | | | , | ٥ . ک | | |
| old up ir R | 3.04 | | | | | | | | | | | | | | | (| 0.92 | | | | | | | | 1.92 | | |
| s: 2-fold up R R 2 | 1.48 | | | | | | | | | | | | | | | | 1.91 | | | | | | | | 96.0 | | |
| n genes R F | 8.75 1 | | | | | | | | | | | | | | | | 2.96 | | | | | | | | 1.04 | | |
| knowr | 602 | | | | | | | | | | | | | | | | 3463 | | | | | | | | 2773 | | |

| TOR 1.112) KINASE ETAL LIVER E-PROTEIN | (| nitori | · | | _ | | ressed cifically in cells he B-lineage, in e pro-B cells in most pre B | mature B cells, not in plasma s. |
|---|--|---|--|--|--|------------------------------------|--|--|
| 0.00.347 CYTOKINE RECEPTOR CURSOR (EC 2.7.1.112) ROSINE-PROTEIN KINASE EPTOR FLK-2) (FETAL LIVER ASE 2) (TYROSINE-PROTEIN ASE FLT3). | 0.00 .243 MEOBOX TEIN HOX-D3 X-4.1) (MH-19). | 18,88 .598 ptor protein plex AP-2, alpha bunit (Ap2a1); | gi-plasma brane transport icle; intracellular tein traffic; | iates protein ing in the ocytic and late | retory pathways 0.00 12.28 .445 aragine thetase (Asns); scription is | ced by amino and obydrate rivation | 2.56.007 | ociated protein sine kinase; ction in B-phocyte specific sduction hway |
| 00.00 | 0.00 | 0.00 | | | 0.00 | ii | 2.13 | |
| 1.52 | 0.00 | 0.00 | | | 0.00 | | 1.61 | |
| 2.72 | 0.00 | 2.87 | | | 0.00 | | 0.61 | ٠ |
| 0.00 | 55.00 | 0.00 | | | 47.82 | | 0.51 | |
| 8.70 | 3.04 | 1.19 | | | 4.54 | | 0.00 | |
| 0.000 8.70 0.00 2.72 | 0.040 3.04 55.00 | 0.037 1.19 0.00 | | | 0.020 4.54 47.82 | | 0.011 0.00 0.51 | |
| 0.00 | 0.00 00.00 | 0.00 | | | 0.00 | | 0.00 | |
| 0.00 | 0.00 | 0.00 | | | 0.00 | | 0.52 | |
| 00.00 | 0.00 | 0.00 | | | 0.00 | | 2.80 1.39 0.00 | |
| 66.6 | 8.49 | 5.17 | | | 0.48 | | 1.39 | |
| \$ 69. | .05 |).24 | | | 2.71 | | 2.80 | • |
| 2.83 10 | 2.43 10 | 3.57 30.24 5.17 0.00 0.00 0.00 | | | 9.37 62.71 0.48 0.00 | | 2.38 | |
| 1172 2.83 10.69 9.99 0.00 0.00 0.00 | 2049 2.43 10.05 8.49 0.00 | 971 | | | 940 | | 0903 | |

.153

| 0.72 1.25.726 igin (8sg); 019 Mouse gene basigin precursor, | igin signal ursor 1.83.289 itonin (Calc) 0.00.374 ium channel beta uitou bunit (Cacnb2); tage-sensitive ium channels are | ely expressed plexes which e both trogenic and al transduction ctions. 2.05.725 onyl reductase 1 uitou r1);a cytosolic. ber of the aldoreductase group nzymes. uitous enzyme abolize a variety ompounds taining carbonyl ups. |
|---|--|---|
| 0.72 | 0.88 | 0.80 |
| 1.13 | 0.00 | . 88.0 |
| 1.44 | 1.91 | 0.95 |
| 0.87 | 1.84 1.91 0.00 27.69 | 1.47 |
| 0.022 1.04 0.87 1.44 1.13 | 0.025 1.12 1 | 0.005 0.80 1.47 0.95 |
| 0.58 | 6.37 0.00 | 0.52 |
| 0.56 | 0.78 1.33 1.43 0.34 0.58 5.03 16.01 1.89 0.00 0.00 | 2.24 2.14 1.72 0.83 1.05 0.52 |
| 0.00 | 0.34 | 0.83 |
| 1.29 | 1.43 | 1.72 |
| 0.96 | 1.33 | 41.5 |
| 019 1.31 0.96 1.29 0.00 0.56 0.58 | 0.78 5.03 | 2.24 |
| 019 | 991 343 | 9 6 . |

- 76-

| ryogenesis | | r ,endoderm ved tissuas. , sromach, ar II intestine. | | eniber GL12 isculuis factor Fgf-7 |
|--|--|--|--|--|
| 1.17.994 dermal-neural ex 1 9 (Enc1); an y and highly cific marker of ral induction in abratus; encodes len family related tein that is; ENC-nctions as an n-binding protein t may be orrant in the anization of the n cytoskeleton ing neural fate cification and elopment of the | 0.00 .374 structure cific onuclease 1 1); a structure- cific | onuclease, 0.22.148 head box A2 r ,endoderin- a2); trancription ved tissuits. or , stomach, | 1.04 .595 eral transcription or IIH, peptide 1 (62kD | 0.00 . 141 - Kruppel family member GL12 2); 222703 M.musculus tinocyte growth factor Fgf-7 |
| 1.7.1 | 0.00 | 1.34 | 1.08 | 0.00 |
| 69.0 | 7.15 | 0.00 | 0.00 | 0.00 |
| 61.19 | 0.00 | 0.85 | 96'0 | 7.63 |
| 86.0 | 0.00 | 0.019 1.70 1.72 0.85 | 1.69 | 0.031 2.28 21.40 7.63 |
| 1.38 | 0.00 | 1.70 | 0.37 | 2.28 |
| 0.010 1.38 0.98 1.19 | 8.37 14.30 8.47 0.00 0.00 0.00 0.00 0.046 0.00 0.00 0.0 | 0.019 | 0.006 0.37 | 0.031 |
| 0.33 0.4 | . 00.00 | 0.20 | 0.61 | 0.00 00.00 |
| | 0.00 | 0.84 | 0.31 | 0.00 |
| 48.0 | 0.00 | 0.12 | 0.79 | 0.00 |
| 1.02 | 8.47 | 1.46 | 1.38 | 5.39 |
| 1.18 | 4.30 | 1.66 | 1.31 | 33.12 |
| 0.83 1.18 1.02 0.54 0.51 | 8.37 1 | 1.15 1.66 1.46 0.12 | 1.55 1.31 1.38 0.79 | 3.13 33.12 5.39 0.00 |
| 079 | 320 | 409 | 023 | 703 |

| 0.00 . 197-Kruppel family ber GLI3 musculus mRNA | Gli3 protein. 1.53.178 amate cysteine r, embryo se (gamma-amylcysteine thetase), catalytic | lc); 0.00 .236 amate receptor. tropic, AMPA2 ha 2} (Gria2); | 0.00 .116 t shock factor 2 f2)M.musculus NA for heat shock | scripton factor 2. 0.00.291 tion plakoglobin (Jup); one of the teins of desmosornal mentbrane horage site plaques of the ballium and is also acomponent of | 0.00.316 uscsulus mRNA goosecoid eobox. | 0.00.251 | 1.06. <i>950</i> usculus mRNA wnt-8D protein. | 0.00.056 usculus mRNA ologous to S. | 0.44.088 usculus mRNA nancer-trap | 0.00.834 usculus myf-6 e. |
|--|--|--|--|---|---|----------------------|--|--|-----------------------------------|------------------------------|
| 1.27 | 1.30 | 0.00 | 0.00 | 0.00 0.00 | 0.00 | 0.00 | 2.19 | 00.00 . 00.00 | 0.68 | 0.00 |
| 0.00 | 0.91 | 0.00 | 0.00 | 1.09 | 0.00 | 0.00 | 0.70 | 0.00 | 0.00 | 8.19 |
| 1.26 | 96.0 | 28.66 | 0.00 | 0.37 | 0.00 26.67 | 0.00 | 0.91 | 38.64 | 4.66 | 2.91 |
| 0.75 | 1.04 | 1.7.1 | 18.64 | 0.91 | 0.00 | 2.14 | 1.73 | 13.92 | 0.74 | 2.53 |
| 1.44 | 0.74 | 5.05 | 7.98 | 2.69 | 2.55 | 9.71 | 1.42 | 3.72 | 4.85 | 0.86 |
| 0.016 1.44 0.75 1.26 | 0.002 0.74 1.04 0.96 | 0.039 5.05 1.71 28.66 | 0.002 7.98 18.64 0.00 | 0.013 2.69 | 0.022 2.55 | 0.032 | 0.041 1.42 | 0.046 3.72 13.92 38.64 | 0.047 4.85 | 0.043 0.86 |
| 0.00 | 0.66 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 13.02 | 0.55 | 0.00 | 0.00 1.26 | 0.00 |
| 0.59 | 0.87 | 0.00 | 0.00 | 1.29 | 0.00 | | 0.0 | 0.00 | | 0.00 |
| | 0.70 | | 0.00 | 0.00 | 0.00 | 0.00 | 1.46 1.95 0.65 | 6.58 0.91 0.00 | 4.23 1.66 0.55 | 0.18 |
| 2.59 | 1.46 | 4.96 | 1.98 | 2.79 | 7.04 | 8.21 | 1.95 | 0.91 | 1.66 | 1.65 |
| 1.99 2.59 0.00 | 1.76 | 2.45 | 5.43 | 2.48 2.79 0.00 1.29 | 13.54 | 1.17 17.10 8.21 0.00 | | 6.58 | 4.23 | 3.39 1,14 1.65 0.18 |
| 1.25 | 1.47 1.76 1.46 0.70 0.87 0.66 | 5.92 22.45 4.96 0.00 | 9.29 15.43 1.98 0.00 | 2.12 | 5.76 13.54 7.04 0.00 | 1.17 | 0.94 | 6.71 | 4.93 | 3.39 |
| 255 | 498 | 498 | 754 | 0365 | 239 | 778 | 889 | 962 | 942 | 090 |

| 0.00,096 usculus SOX1 e.)PIR:S10950 -determining tein - mouse | 0.00 .2733453 Mouse somal protein (rpl.32') gene, | 0.00 .794 tocytoma N-deacetylase/N- otransferase (Mndns); usculus mRNA for glucusamiityl | eacatylasa / N-Sunoviansteinso. 0.00 .144 rine Hox 2.2 NA for a | 60.73.012s musculus 5E6 6/Ly-49C) mRNA, | plete cos. 0.00.420s musculus in-2 mRNA, | ial cos. 1.04.053s musculus tocyst unknown tein mRNA, partial | 0.73.143s musculus cea 17 e. | 2.48 .913s musculus erbB2 NA, partial cds. | 0.80.557s musculus ne/threonine | tein kinase 4m (PRP4m) NA, complete cds |
|---|---|--|---|--|--|--|---------------------------------|---|------------------------------------|---|
| 0.69 | 0.00 | 1.16 | 1.19 | 0.71 | 0.00 | 0.55 | 0.04 | .0.79 | 1.27 | |
| 0.97 | 0.00 | 2.69 | 0.00 | 0.76 | 4.26 | 0.81 | 1.27 | 0.68 | 1.41 | |
| 2.14 | 2.36 | 5.53 | 0.81 | 1.38 | 0.00 | 1.18 | 1.36 | 1.01 | 0.00 | |
| 1.03 | 4.23 | 0.00 | 1.84 | 1.72 | 0.00 00.00 | 1.14 | 1.29 | 1.34 | 0.041 1.26 1.33 0.00 | |
| 1.35 | 9.94 | 0.00 | 1.26 | 1.18 | 3.70 | 1.26 | 1.32 | 1.82 | 1.26 | |
| 0.003 1.35 1.03 2.14 | 0.009 9.94 4.23 2.36 | 0.046 0.00 | 0.015 1.26 1.84 0.81 | 0.019 1.18 1.72 1.38 | 0.036 3.70 | 0.032 1.26 1.14 1.18 | 0.025 1.32 1.29 1.36 | 0.029 1.82 1.34 1.01 | 0.041 | |
| 0.00 | 0.00 | 0.00 | 0.00 | 0.57 | 0.00 | 0.75 | 0.19 | 99.0 | 0.00 | |
| 0.00 0.00 | 0.00 | 0.84 | 0.00 0.00 | 0.25 | 0.0 | 0.28 | 0.00 | 0.00 | 0.76 | |
| 8.0 | 0.00 | 0.20 | 0.40 | 0.86 | 9.34 6.07 0.00 | 0.71 | 0.65 | 1.15 0.99 0.48 | 0.87 1.16 0.00 | |
| 1.44 | 7.19 | 2.44 | 1.27 | 1.53 | 6.07 | 96.0 | 1.18 | 0.99 | 1.16 | |
| 1.55 | 0.32 | 1.23 | 1.67 | 1.14 | 9.34 | 1.27 | 1.16 | 1.15 | 0.87 | |
| 2974 2.34 1.55 1.44 0.00 | 1453 6.48 30.32 7.19 0.00 0.00 '0.00 | 1.34 1.23 2.44 0.20 0.84 0.00 | 2.63 1.67 1.27 0.40 | 1617 1.41 1.14 1.53 0.86 | | 2762 1.25 1.27 0.96 0.71 | 3262 0.84 1.16 1.18 0.65 | 1.51 | 1.13 | |
| 2974 | 1453 | 885 | 461 | 1617 | 2456 1.22 | 2752 | 3262 | 2465 | 737 | |

| 0.88 . <i>168</i> s musculus SH3· taining protein P3 mRNA, partial | 0.00 14.09,177s musculus I/SNF complex 60 subunit (BAF60 | 0.97 .607s musculus scription factor 4 (tbx4) mRNA, ial cds. | 3.51 . <i>076</i> s musculus scription factor 2. (USF2) gene | 0.00 30.03 .826s musculus zinc er protein (kid-1) e, complete cds. | 6.55 . 144 assium voltage-gated channel, family H (eag-related), member 2 nh2); Mus musculus ether a-go- | elated protein isoform Merglä rg1) mRNA, complete cds. 1.91 . 189 roenkephalin 2 alls k2);a homolog of brain | roenkephalin, a rotransmitter 0.00 . 119 collagen, type IX, alpha o19a1); a fibrillar collagen, the ely distributed elements of the acellular matrix. | 2.18 . <i>558</i> collagen, type VI, a 1 (Col6a1); 0.94 . <i>057</i> kinje cell protein 4 n 4); |
|--|--|---|--|--|--|--|--|--|
| 0.47 | 0.00 | 1.64 | 1.99 | 0.00 | 3.26 | 1.78 | 0.00 | 0.00 |
| 0.99 | 8.09 | 0.62 | 1.49 | 0.00 | 0.18 | 0.61 | 0.00 | 0.00 |
| 1.01 | 0.00 | 1.09 | 0.31 | 0.00 | 0.00 | 0.63 | 43.25 | 0.30 2.07 |
| 1.14 | 0.52 | 1.47 | 0.85 | 19.06 | 0.00 | 0.95 | 51.41 | 0.036 1.52 0.30 2.07 0.009 1.20 1.30 1.06 |
| 1.02 | 1.48 | 1.21 | | 2.78 | 0.00 | 0.70 | 0.00 | 1.52 |
| 0.002 1.02 | 0.023 1.48 | 0.043 1.21 1.47 1.09 | 0.048 1.15 | 0.001 2.78 19.06 | 0.038 0.00 0.00 | 0.031 0.70 0.95 | <i>0.001</i> 0.00 51.41 43.25 | 0.036 1.52 0.009 1.20 |
| 0.51 | 60.09 | 0.80 | 0.52 | 0.00 | 1.82 | 0.22 | 0.00 | 0.06 |
| 0.83 | 0.00 | 0.18 | 0.45 | 0.00 | 0.00 1.82 | 1.05 | 0.00 | 0.88 |
| 0.55 | 9.81 3.90 0.00 0.00 0.09 | 0.37 | | 0.00 | 3.25 3.67 2.03 0.00 | 0.60 | 2.63 30.79 0.41 0.00 | 1,12 1,22 1,32 0.00 0.88 1,15 1,31 1,26 0.00 0.44 |
| 1.40 | 3.90 | 1,23 | 1.93 | 8.56 | 2.03 | 1.47 | 0.41 | 1.32 |
| 1.60 | 9.81 | 1.03 1.23 0.37 | 0.80 1.93 0.11 | 13.60 | 3.67 | 1.40 | 30.79 | 1.22 |
| 1.50 1.60 1.40 0.55 0.83 | 1.83 | 2078 0.90 | 2.27 | 1.20 13.60 8.56 0.00 | 3.25 | 1.35 1.40 1.47 0.60 1.05 0.22 | 2.63 | 1.12 |
| 883 | 620 | 2078 | 283 | 247 | 128 | 3227 | 2136 | 405 |

| 0.00.374 21 homolog (S. pornibe) d21); D49429 Mouse P-29 mRNA for PW29, | plate cus 1.10.750 -related orphan -t, nuiscle, ptor gamma - ey, brain, luig, rcl; is, and spleon. | 1.04.634 binding motif tein 4 (Rbm4): | 0.05.461 0 calcium-binding protein A13 00a13); M.musculus mRNA for 0 calcium-binding protein A13. | 0.00.341 solute carrier family 1, member c. (SIc1a6); a Purkinje cell specific | 1.15.247 ocerebellar staxia 1 hamolog an) (Sca1) M.musculus inRNA | ataxin-1. 0.00.360ell expressing clone j6 (Yj6); usculus J687 mRNA for T cell | 0.00 . 117 is specific X- ed gene (Tsx): | 1.46.6261 cytotoxic ule-associated | -binding protein- 1 (Tal1); | ptosis 2.07 .872 scriptional rmediary factor loha (Tif1a): | 0.00.213 sient receptor tein 1 (Trrp1); | 2.33 .407 oil factor 2 (spasmolytic protein Tff2); M.musculus spasmolytic peptide (SP) mRNA. |
|---|--|--|---|--|---|---|---|---------------------------------------|--------------------------------|---|--|--|
| 0.00 | 1.08 | 1.61 | 1.38 | 1.70 | 0.71 | 0.00 | 0.00 | 1.00 | | 0.46 | 0.01 | 0.00 |
| 0.00 | 0.80 | 0.20 | 0.00 | 0.26 | 0.00 | 2.67 | 0.00 | 0.63 | | 0.40 | 1.60 | 0.00 |
| 0.00 | 1,45 | 0.07 | 2.28 | 2.37 | 1.68 | 2.35 | 0.00 | 0.65 | | 0.97 | 1.51 | 0.00 |
| 0.00 | 0.83 | | 0.00 | 0.55 | 1.61 | 0.00 | 24.48 | 1.00 | | 1.03 | 1.26 | 3.07 |
| 0.64 | 0.92 | 0.34 | 1.10 | 1.45 | | 3.50 | 2.27 | 1.02 | | 1.20 | 1.23 | 2.71 |
| 0.047 0.64 0.00 0.00 | 0.021 0.92 0.83 1.45 | 0.044 0.34 1.51 | 0.001 1.10 | 0.003 1.45 | 0.020 0.57 | 0.013 3.50 | 0.000 2.27 24.48 | 0.013 1.02 1.00 | | 0.029 1.20 1.03 | 0.032 1.23 | 17.2 100.0 |
| 0.00 | 0.70 | 0.12 | 0.00 | 0.17 | 0.00 | 0.00 | 00.00 | 0.88 | | 0.00 | 0.64 | 0.00 |
| 0.00 | 0.26 .0.70 | 0.78 | 0.90 | 0.22 | 0.00 | 0.00 | 0.00 | 0.81 | | 0.80 | 0.14 | 0.00 |
| 5.19 0.00 | | 96.0 | 0.31 | 0.33 | 0.85 | 0.00 | 8.91 0.00 | 0.82 | | 0.43 | 0.20 | 0.00 |
| .19 | 1.12 | 1.34 | 2.49 0.31 | 2.52 | 1.42 | 8.97 | 8.91 | 2.44 | | 1.18 | 1.38 | 3.28 |
| | 1.10 1.20 1.12 0.73 | 1.49 1.34 0.96 | 2.75 | 2.20 2.52 0.33 | 1.23 1.42 0.85 | 8.76 8.97 0.00 | 8.76 | 1.65 2.44 0.82 | | 1.12 | 0.77 1.50 1.38 0.20 | 3.62 3.28 0.00 |
| 4.85 13.23 | 1.10 | 2.15 | | 3.53 | 1.58 | 1.22 | 1.68 | 2.82 | | 4429 1.32 1.12 1.18 0.43 | 0.77 | 2.55 |
| 429 | 170 | 506 | 921 | 262 | 542 | 184 | 796 | 861 | | 4429 | 167 | 697 |

| 0.97 .707 sine kinase ptor-1 (Tiel); usculus mRNA TIE receptor sine kinase. 1.06 .700 297 Mus · | chrome Bbo I yt) mRNA, plete cds 0.00.099 399 Mus culus Cdk- bitor p57KIP2 | plete cds 1.08.111 788 Human ative cytochroine c- | e syntnatase NA, complete cds 1.88. <i>014</i> 818 Mus culus tuberin C2) mRNA, | plete cds 0.00.871 925 Mus culus scription factor mRNA, complete | 8.39.645 OB5 Mus culus thiazide- sitive Na-Cl ransporter mRNA. | plete cds 0.00 215.85 .460 673 Mus musculus histone (A)-613, histone H2a(B)-61: one H2b-613 (H2b) genes, plete cds |
|---|--|--|--|--|---|--|
| 3.78 | 0.00 | 0.00 | 2.13 | 1.83 | 0.00 | 00:00 |
| 3.37 | 00.0 | 0.35 | 1.45 | 1.27 | 0.00 | 0.00 |
| 1.01 | 9.23 | 1.93 | 0.51 | 1.49 | 1.56 | 0.00 |
| 0.00 1.18 | | 0.92 | 0.68 | 1.13 | 1.24 | 0.00 |
| .26 | 1.45 4 | 1.25 | | | | |
| 0.015 1.03 0.00 1.18 0.001 1.26 1.32 1.01 | 0.001 4.45 42.28 | 0.003 1.25 | 0.043 1.07 | 0.012 0.13 | 0.020 1.40 | 0.028 6.97 |
| 0.14 | 0.00 | 0.00 | 0.52 | 0.50 | 0.47 | 0.00 |
| 0.00 0.14 | 0.00 | 0.00 | 0.09 | 0.50 | 0.00 | 0.00 |
| | 0.00 | | | 0.43 | 0.00 | 2.34 |
| 0.84 (| 5.57 | 2.04 | 0.93 | 0.87 | 0.76 | 2.46 |
| 1.22 0.84 0.00 | | 1.19 2.04 0.00 | 1.21 0.93 0.79 | 1.33 0.87 0.43 | 1.51 0.76 0.00 | 5.66 |
| 1.87 1.22 0.84 0.00 0.99 1.46 1.35 0.00 | 6.64 22.65 | 1.60 | 1.30 | 1.35 | 1.43 | 2.43 25.66 2.46 2.34 |
| 960 | 399 | 788 | 818 | 925 | 085 | 673 |

ġ -

| 2.39 . <i>928</i> 849 Mouse kFGF genomic | 0.97, 080 998 M.musculus for gamma 2c 1.56,236 438 Mouse MP4 e for a proline | 0.00 .051 398 Mouse Flt3 NA for tyrosine se receptor of PDGF | 1,00 . <i>106</i> 091 M.musculus mRNA | 0.27 . 177 719 Mus culus CREB gene cAMP-responsive- | ent binding tein, exon 2 0.82.052 904 M.musculus AST mRNA for T receptor alpha | in 6.28.931 850 M. culus mRNA for P kinase | vated protein se 2 0.00 . 175 104 M.musculus NA for ali2 gene | 0.00 .374 aguchi sarcoma I (v-yes) ogene homolog | s); 0.82. <i>079</i> 509 Mouse NA for PAP ologous protein |
|---|---|---|--|---|--|---|--|--|--|
| 0.29 | 0.00 | 0.00 | 0.00 | 0.00 | 0.07 | 1.48 | 0.00 | 0.00 | 0.00 |
| 0.80 | 0.24 | 0.00 | 0.41 | 1.16 | 00.00 | 0.00 | . 00.0 | 0.00 | 0.72 |
| 0.94 | 1.51 | 4.19 | 1.05 | 1.19 | 1.04 | 0.52 | 0.00 | 0.00 | 2.33 |
| 0.58 | 1.38 | | 1.19 | 0.84 | 3.00 | 8.14 | 0.029 6.59 11.41 | 0.008 0.00 79.97 | 0.037 1.18 1.23 |
| | 0.80 | 9.14 | 1.00 | 1.25 | 1.97 | 0.00 | 6.59 | 0.00 | 1.18 |
| 0.039 1.76 | 0.022 0.83 0.000 0.80 | 0.007 9.14 12.37 | 0.027 1.00 1.19 | 0.000 1.25 | 0.039 1.97 | 0.001 0.00 | 0.029 | 0.008 | 0.037 |
| 0.00 | 0.36 | 0.00 | 0.67 | 0.13 | 0.00 | 0.00 | 0.00 | 0.00 | 0.72 |
| 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.96 | 0.00 | 0.00 | 0.00 | 0.00 |
| 1.06 | 1.03 | | 0.54 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 2.10 1.26 0.46 |
| 1.17 | 1.29 | 5.19 | 1.06 | 1.41 | 1.39 | 1.83 1.79 0.00 | 7.66 | 4.42 | 1.26 |
| 2.41 1.17 1.06 | 1.67 | 4.55 | 1.09 1.23 1.06 0.54 | 1.51 1.33 1.41 0.00 | 2.04 1.39 0.00 | | 7 27 7 66 0.00 | 3.74 25.02 4.42 0.00 | |
| 2.21 | 1.75 1.67 1.29 1.03 0.65 0.36 1.25 1.54 1.20 0.00 0.00 0.00 | 8.81 54.55 5.19 0.00 | 1.09 | 1.51 | 1.21 | 2.50 | 4 | 3.74 | 1.18 |
| 849 | 998 | 398 | 091 | 719 | 904 | 860 | Ş | 677 | 509 |

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| 1.20.952 use mRNA for ase small unit, complete | 2.64.657 801 Mouse NA for Emb, | 0.90 .398 095 Mouse DNA histamine H1 ptor, complete | 0.00.099 471 House se; Musculus esticus testis NA for gsg3, | plete cds 0.00.357 900 House se; Musculus esticus male | 0.08.199 | 0.00.0651 | 0.31 . <i>078</i> |
|--|-----------------------------------|---|--|--|------------------|------------------|-------------------|
| 0.19 | 0.00 | 1.25 | 00.00 | 1.39 | 0.00 | 0.00 | 00.00 |
| 1.25 | 0.00 | 0.85 | 0.00 | 0.00 | 0.00 | 0.00 | 1.06 |
| 1.14 | 0.59 | 1.00 | 17.72 | 0.82 | 1.84 | 7.89 | 0.94 |
| 1.04 | 2.04 | 2.10 | 27.48 1 | 0.043 0.63 1.81 0.82 | 0.000 6.27 25.66 | 14.39 | 1.46 |
| 0.54 | | 1.00 | 2.16 | 0.63 | 6.27 | 2.92 | 1.73 |
| 0.039 0.54 1.04 1.14 | 0.000 1.41 | 0.002 1.00 2.10 1.00 | 0.027 2.16 27.48 17.72 | 0.043 | 0.000 | 0.000 2.92 14.39 | 0.000 1.73 |
| 0.34 | 0.00 | 0.15 | 00.0 | 1.18 | 0.00 | 0.00 | 0.00 0.00 |
| 0.21 | 0.0 | 0.14 | 0.00 | 0.00 | 0.16 | 0.00 | 0.0 |
| 0.83 | | 0.52 | | 90.0 | 67 0.00 | 0.00 | .43 0.25 |
| 1.67 | 1.93 | 1.43 | 8.38 0.00 | 1.86 | ထ် | 5.50 7.16 0.00 | - |
| 1.28 | 1.90 | 1.23 | 27.16 | 1.66 | 18.86 | 5.50 | 1.60 |
| 0.96 1.28 1.67 0.83 | 1.99 1.90 1.93 0.00 | 1.34 1.23 1.43 0.52 | 5.32 27.16 | 1.35 | 6.21 18.86 | 5.84 | 1642 1.28 |
| 544 | 108 | 960 | 471 | 900 | . 146 | 1090 | 1642 |

| 1.07.065 ILORIDE-SENSITIVE SODIUM NNEL ALPHA-SUBUNIT (LUNG CHANNEL ALPHA SUBUNIT) PHA ENAC) (NONVOLTAGE: TED SODIUM CHANNEL 1 ALPHA UNIT) (SCNEA) (ALPHA NAC!!) | AGMENT). 1.09.104s musculus ant formin (Fmn) | 0.94 .031s musculus t10b mRNA, | 0.94.060s musculus Sox4 x4) mRNA, partial | 0.00 . 182s musculus Sox 12 x12) mRNA. | lal Cos. 1.22. <i>105</i> s musculus Mad olog Smad5 NA, complete | 0.26.900use hyaluronan thase 3 mRNA, | 1.21.153 usculus mRNA dystrobrevin ne m32). | 0.00.487 usculus mRNA phospholipase C | 0.00.086 | 0.90.515 |
|--|--|-----------------------------------|--|---|---|---|---|--|------------|----------------|
| 0.00 | 0.45 | 96.0 | 1.14 | 0.00 | 0.23 | 1.07 | 0.01 | 5.28 | 1.43 | 0.74 |
| 0.00 | 0.29 | 0.55 | 0.00 | 00.00 | 0.00 | 1.76 | 0.51 | 3.07 | 0.00 | 1.33 |
| 0.93 | 1.32 | 1.36 | 2.08 | 0.29 | 3.46 | 0.70 | 1.34 | 1.35 | 1.93 | 1.52 |
| 2.79 | 0.91 | 1.68 | 1.71 | 15.36 | 2.67 | 0.41 | 1.08 | 2.97 | 1.55 | 1.19 |
| 2.77 | | 1.23 | 1.41 | 9.16 | 0.80 | 1.74 | 1.19 | 0.00 | 1.39 | 0.84 |
| 0.000 2.77 | 0.019 1.42 | 0.002 1.23 | 0.037 1.41 | 0.000 9.16 15.36 | 0.016 0.80 | 0.033 1.74 | 0.001 1.19 | 0.018 0.00 | 0.033 1.39 | 0.021 0.84 |
| 0.00 | 0.24 | 0.00 | 0.00 | 0.00 | 0.40 | 0.00 | 0.00 | 0.00 | 0.00 | 0.52 |
| 00.00 | 0.47 | 0.00 | 0.00 | 0.00 | 0.00 | 0.93 | 0.00 | 0.00 | 0.39 | 0.51 |
| 4.44 0.00 | | 1.04 0.00 | 0.98 0.00 | 0.00 | 1.81 0.60 | 0.35 | 1.36 0.07 | 0.00 | 1.47 0.00 | 1.18 0.62 |
| 4.44 | 1.09 0.84 | 1.04 | 0.98 | 8.98 | 1.81 | 1.28 | 1.36 | 0.81 | 1.47 | 1.18 |
| 3.39 | 1.55 | 1.67 | | | 1.21 | 1.58 | 1.07 | 1.19 | 1.69 | 1.77 |
| | 1.51 | 1.20 | 2.44 1.02 | 9.81 | 1.20 | 1.24 | 0.93 | 1.98 | 0.61 | 1.10 |
| 1677 3.66 | 2211 1.51 | 2229 1.20 | 2444 | 2446 9.81 28.01 | 2570 1.20 1.21 | 2673 1.24 | 2998 0.93 | 3005 1.98 | 3019 0.61 | 3122 1.10 1.77 |
| | | | | | | | | | | |

| 1.15. <i>331</i> usculus htlf e, exon. | 1.60 .370 OPAIN PRECURSOR (EC 3.4 22) STEINE PROTEASE CPP32) MA PROTEIN) (CASPASE-3) | E). 0.46. <i>065</i> usculus mRNA semaphorin Hv 88 bol | 1.19.207s musculus A· protein (A-myb) | 0.00 .335 use skeletal | sphorylaso se, gamma unit mRNA, | plate cds 0.36. <i>095</i> 298 Mouse rine orransferrin | NA 0.00 , 159 060 Mouse somal protein, e 3A coding for | 0.00 . 138 use mRNA ced by PDGF h some homology | -10s. 0.23.654 s musculus erentiation igen (CD22) NA, complete | 0.77 .458 472 Mouse Bax a mRNA, plete cds |
|---|--|---|--|------------------------|---------------------------------------|---|---|---|--|---|
| 0.79 | 0.63 | 0.95 | 0.00 | 2.35 | | 0.80 | 0.00 | 1.40 | 0.55 | 0.35 |
| 0.47 | 0.52 | 0.04 | 0.29 | 8.26 | | 0.94 | 0.00 | 0.65 | 1.79 | 1.50 |
| 1.05 | 1.23 | 1.25 | 1.00 | 0.00 | | 1.06 | 0.00 | 1.04 1.75 | 0.00 | 0.70 1.23 |
| 0.98 | 1.02 | 1.19 | 1.11 | 2.18 | | 1.08 | 7.47 | 1.04 | 0.00 | 0.70 |
| 1.02 | 1.69 | 1.05 | 1.00 | 0.00 | | 1.64 | 3.72 | 2.30 | 5.18 | 0.004 1.84 |
| 0.006 1.02 | <i>0.001</i> 1.69 | 0.009 1.05 1.19 1.25 | 0.001 1.00 1.11 1.00 | 0.001 0.00 | | 0.046 1.64 | 0.002 3.72 | 0.027 2.30 | 0.027 5.18 | 0.004 |
| 0.64 | 0.39 | 0.00 | 0.18 | 0.00 | | 0.89 | 0.00 | 0.00 | 0.00 | 0.00 |
| 0.30 | 0.45 | 0.58 | 0.17 | 0.00 | | 0.76 | 0.00 | 0.26 | 3.91 3.04 0.00 1.45 | 0.52 |
| | | 0.36 | 0.43 | 0.00 | | 1.49 1.34 0.00 | 7.40 5.77 2.15 | 0.96 1.61 0.73 | 0.00 | 1.81 1.41 0.00 |
| 1.06 | 98.0 | 1.69 | 1.14 | 2.41 | | 1.34 | 5.77 | 1.61 | 3.04 | 1.41 |
| 1.26 1.06 0.59 | 1.17 0.98 0.61 | 1.60 1.69 0.36 | 1.34 1.14 0.43 | 8.72 10.87 2.41 0.00 | | 1.49 | 7.40 | 0.96 | 3.91 | 1.81 |
| | | | 1.25 | 8.72 | | 1.25 | 6.51 | 1.75 | 2.01 | 1.38 |
| 3226 1.13 | 3241 1.07 | 3410 1.13 | 3528 | 293 | | 298 | 090 | 785 | 928 | 472 |

| 0.00 .299 167 Mouse zinc er protein mRNA · | 0.00 . 132 580 Mus culus galanin | e 0.20. <i>052</i> 567 Mus culus antigen, B- receptor gene, | plete cds 1.30.2210114 Mouse pa-casein mRNA, | plete cds 0.97 , <i>137</i> 6395 Mouse a-fetoprotein | P) gene 0.00 .425use interleukin 2) gene, exon 4 | 0.34.0772740 Mouse rotropin beta- | 0.00 . 1823501 Mus musculus secreted T protein (P500/TCA3; SIS-spsilon) | NA, complete Cos 1.06.3568449 Mouse Hux- protein mRNA, | nd 0.96. <i>070</i> 9015 Mouse somal protein L7 | 7) gene. plete cds 0.92 . 1799395 Mouse tidine-5'- | opnospnate arboxylase NA, 3' end |
|---|-------------------------------------|--|--|--|---|-----------------------------------|---|--|---|---|--|
| 1.86 | 0.00 | 0.76 | 0.89 | 0.91 | 0.00 | 1.01 | 1.85 | 0.44 | 0.81 | 1.08 | |
| 00.0 | 00.00 | 0.14 | 0.00 | 0.10 | 1.28 | 0.00 | 0.00 | 1.02 | 0.75 | 0.08 | |
| | | | | 1.03 | 4.12 | 1.46 | 6.56 | 0.95 | 1.29 | 2.66 | |
| 96.0 | 2.38 1 | 3.25 1.24 | 1.34 | 1.18 | 0.72 | 0.99 | 0.15 | 1.16 | 1.44 | | |
| 1.89 | 7.22 4 | | 1.24 | | | | | 1.07 | 1.17 | 1.63 | |
| 0.008 1.89 0.95 1.43 | 0.004 7.22 42.38 12.47 | 0.000 4.39 | 0.030 1.24 1.34 1.29 | 0.001 1.83 | 0.013 0.00 | 0.012 1.21 | 0.015 2.02 | 0.000 1.07 | 0.019 1.17 1.44 1.29 | 0.018 1.63 1.09 | |
| 0.00 | 0.00 | 0.03 | 0.18 | 0.48 | 0.00 | 0.15 | 0.00 | 90.0 | 0.09 | 0.00 | |
| 0.00 | 0.00 | 0.10 0.03 | 0.75 | 0.00 | 1.37 | 0.43 | 0.00 | 0.00 | 0.39 | 0.00 | |
| | | 3.79 0.00 | 0.08 | | 2.65 4.76 0.00 | 0.79 | 8.25 3.49 0.00 | 0.98 1.20 0.00 | 0.69 | 0.00 | |
| 1.67 | 9.09 | 3.79 | 0.96 | 1.58 | 4.76 | 1.36 | 3.49 | 1.20 | 1.04 | 2.00 | |
| 1.39 | 8.21 | 3.57 | 1.04 | 1.38 | 2.65 | 1.33 | 8.25 | 0.98 | 1.14 1.04 0.69 | 1.38 2.00 0.00 | |
| 1.05 1.39 1.67 0.51 | 2.58 18.21 9.09 0.00 | 2.83 | 1,16 1.04 0.96 0.08 | 1.56 1.38 1.58 0.00 | 4.79 | 2740 1.19 1.33 1.36 0.79 | 5.31 | 1.03 | 9015 1.49 | 0.76 | |
| 167 | 280 | 567 | 0114 | 6395 | 6762 | 2740 | 3501 | 8449 | 9015 | 9395 | |

| 1.46 1.02 1.30 1.55 1.09 1.27 5.22 6.29 3.99 3.14 1.13 0.78 1.23 1.00 1.27 1.33 1.76 0.98 | 1.52 0. 2.18 0. 1.57 0. 1.30 0. 1.20 0. | | | 0.00 0. | 0.030 1 0.005 1 0.038 3 0.032 0 0.032 0 | | 1.48 1.05 1.09 6.22 6.22 0.34 0.34 | 0.98 1.46 1.28 1.28 1.65 1.165 | 0.32 0.33 0.00 0.00 0.00 0.00 0.00 1.00 | 1.12 0.79 1.10 1.10 1.125 1.25 1.32 2.00 | 0.00. 1720441 Mouse onless potassium nnel gene MK3 0.95. 0520644 Mouse ic fibroblast wit factor (Fgtb) NA, complete cds 0.91.4274094 Mouse noic acid- onsive protein 1 gene, complete culus mouse t cell protease-4 NA, complete cds 0.38. 1055875 Mouse C class I T3-d e (H-2-d lotype) 1.17.997 1591 Murine 0 neutral opeptidase 24.11 10/NEP) mRNA, ative cds r protein MP70 50) gene, plete cds 1.41. 770 1243 Mouse lens r protein MP70 50) gene, plete cds 1.48. 067 3128 Mouse eobox protein X21 mRNA, plete cds 1.62. 102 989 Nkx-5.2 = NK-related eobox gene (mice, E11.5 ryos, mRNA Partial, 148. |
|---|--|--|--|---|---|--|--|--|---|--|---|
| 9 0 6 7 6 8 7 9 | 1.02 1.56 1.27 1.27 0.78 0.78 0.78 | 1.55 1.52 0. 1.55 1.52 0. 1.27 2.18 0. 3.14 3.34 0. 0.78 1.30 0. 1.00 1.00 0. 1.33 1.20 0. | 1.55 1.52 0.87 1.55 1.52 0.87 1.27 2.18 0.00 6.29 1.57 0.00 3.14 3.34 0.00 1.00 1.00 0.00 1.33 1.20 0.89 1.33 1.20 0.89 | 0.08 0.00 0.00 0.00 0.00 0.00 | | 0.08 0.50 0.42 0.61 0.46 0.00 0.00 0.00 0.00 0.00 0.00 0.59 0.00 0.00 0.00 0.00 | 0.08 0.50 0.030 1.08 0.42 0.61 0.005 1.47 0.46 0.00 0.022 0.45 0.00 0.00 0.038 3.23 0.00 0.00 0.025 1.02 0.00 0.00 0.032 1.00 0.24 0.00 0.024 0.59 | 0.08 0.50 0.030 1.08 0.42 0.61 0.005 1.47 0.46 0.00 0.022 0.45 0.00 0.00 0.038 3.23 0.00 0.00 0.025 1.02 0.00 0.59 0.034 1.22 0.00 0.00 0.024 0.59 | 0.08 0.50 0.030 1.08 1.48 0.42 0.61 0.005 1.47 1.05 0.06 0.00 0.022 0.45 1.09 0.00 0.00 0.038 3.23 6.22 0.00 0.00 0.025 1.02 0.98 0.00 0.59 0.014 1.22 0.34 0.00 0.00 0.032 1.00 0.77 | 0.08 0.50 0.030 1.08 1.48 0.98 0.42 0.61 0.005 1.47 1.05 1.46 0.46 0.00 0.022 0.45 1.09 1.97 0.00 0.00 0.038 3.23 6.22 0.93 0.00 0.00 0.025 1.02 0.98 1.28 0.00 0.00 0.032 1.00 0.77 0.78 0.24 0.00 0.024 0.59 0.79 1.16 | 0.08 0.50 0.030 1.08 1.48 0.98 0.39 0.42 0.61 0.005 1.47 1.05 1.46 0.32 0.46 0.00 0.022 0.45 1.09 1.97 0.00 0.00 0.00 0.038 3.23 6.22 0.93 0.00 0.00 0.00 0.025 1.02 0.98 1.28 0.39 0.00 0.00 0.032 1.00 0.77 0.78 1.00 0.24 0.00 0.024 0.59 0.79 1.16 1.02 |

| 0.97 .181s musculus ofetal antigen | NA, partial cas 0.00 . <i>054</i> 982 Mus culus Balb/c roendothelin-1 | e, promoter on 0.00. <i>080</i> 210 Mus culus oelastin mRNA. | plete cds 1.32.313 932 Mus musculus follicle ulating hormone beta subunit | 1.82.480 443 Mus culus proto- | ogene protein C. (c-ros) mRNA. plete cds 0.73.114 252 Mus culus aborropic amate receptor 8 | plete cds plete cds 0.12.067 513 Mus culus KRAB-zinc er protein 79 79) mRNA, | ial cds 0.00 .412s musculus tbc1 NA, complete cds | 0.00 . 145 245 Mus culus fos-related igen-1 (Fra-1) NA, complete cds |
|---------------------------------------|--|--|---|-------------------------------|--|---|---|---|
| 0.67 | 1.02 | 0.00 | 0.80 | 0.70 | 1.09 | 66.0 | 0.00 | 1.24 |
| 1.41 | 00.00 | 0.00 | 0.00 | 0.13 | 0.95 | 00.00 | 7.06 | 0.00 |
| 1.35 | 0.98 | 14.29 | 0.87 | 1.21 | 1.34 | 1.12 | 9.70 | 1.1 |
| 1.29 | 2.53 | 4.29 14.29 | 1.30 | 1.51 | 1.05 | 1.29 | 0.043 0.00 7.73 | 0.007 1.21 1.16 1.11 |
| 1.49 | | 6.61 | 1.40 | 1.1 | 1.19 | 1.09 | 0.00 | 1.21 |
| 0.009 1.49 1.29 | 0.000 2.28 | 0.012 6.61 | 0.024 1.40 1.30 | 0.001 1.11 1.51 1.21 | 0.002 1.19 1.05 1.34 | 0.029 1.09 1.29 1.12 | 0.043 | 0.001 |
| 0.35 | 0.28 | 0.00 | 0.48 | 0.03 | 0.32 | 0.72 | 0.00 | 0.00 |
| 0.21 | 0.21 0.28 | 5.68 14.95 9.70 0.00 0.00 0.00 | 0.16 | 0.07 | 0.20 0.32 | 0.18 | 0.00 | 0.00 |
| 0.00 | 1.71 1.86 0.42 | 0.00 | 0.86 | 0.89 1.26 0.00 | 1.07 1.19 0.00 | 1,45 1.29 0.68 | 3.41 10.25 4.71 0.00 | 0.89 1.28 1.19 0.00 |
| 0.83 | 1.86 | 9.70 | 1.28 | 1.26 | 1.19 | 1.29 | 4.71 | 1.19 |
| 1.38 | 1.71 | 4.95 | 1.13 1.28 0.86 | 0.89 | 1.07 | 1.45 | 10.25 | 1.28 |
| 1.03 1.38 0.83 0.00 | 2.02 | 5.68 1 | 1.42 | 1.24 | 0.92 | 1.01 | 3.41 | 0.89 |
| 662 | 982 | 210 | 932 | 443 | 252 | 513 | 005 | 245 |

| 0.12.105 353 Mus musculus protein sphatase 2A B'alpha3 regulatory unit mRNA, partial cds | 1.74.777 189 Mus musculus pancreatic peptide/neuropeptide Y/peptide receptor gene, complete cds | 0.35.020 650 Mus musculus neurexophilin xph-2) gene, large exon and 3' see the increase and neurial cds | 1.35.150 513 Mus musculus Riversitates ociated, coiled-coil forming protein se p160 ROCK-2 mRNA, complete | 0.00 .123 418 Mus culus Netrin-1 rin-1) mRNA, plete cds | 0.65 .057 137 Mus culus T2· herin mRNA. | ial cds 0.00 .099 208 Mus cultus neurogenin | gn3J gene, plete cds 0.36.054 s musculus serine teinase inhibitor 6 16) mRNA, | plete cds. 0.00.324s musculus ative sphoinositide 5- sphatase type II NA, complete |
|--|---|---|---|--|---|---|---|--|
| 1.07 | 0.83 | 0.85 | 0.99 | 0.51 | 0.97 | 0.00 | 0.00 | 0.00 |
| 0.00 | 1.10 | 0.75 | 1.23 | 1.04 | 0.36 | 0.00 | 0.70 | 0.85 |
| 1.36 | 1.29 | 1.17 | 1.00 | 1.13 | 1.35 | 38.84 | 4.75 | 0.00 |
| 0.99 | 1.23 | 0.009 1.28 1.30 | 1.00 | 0.037 2.23 1.04 1.13 | 0.020 1.73 1.03 | 0.007 8.28 13.48 38.84 | 0.004 5.33 1.30 4.75 | 1.53 |
| 1.07 | 1.40 | 1.28 | 1.02 | 2.23 | 1.73 | 8.28 | 5.33 | 1.15 |
| 0.005 1.07 0.99 1.36 | 0.030 1.40 1.23 1.29 | 0.003 | 0.010 1.02 1.00 1.00 | 0.037 | 0.020 | 0.007 | 0.004 | 0.011 1.15 |
| 0.00 | 0.65 | 0.00 | 0.59 | 0.44 | 0.95 | 0.00 | 0.00 | 0.00 |
| 0.49 | 0.00 | 0.64 | 1.09 1.05 0.51 0.36 | 0.78 | 0.72 | 0.00 | 0.00 | 2.24 |
| 0.00 | | 0.17 | 0.51 | 1.45 1.72 0.00 | 0.00 | 0.00 | 3.18 3.26 0.00 | 5.29 5.43 0.00 |
| 1.30 | 0.86 | 1.17 | 1.05 | 1.72 | 1.58 | 5.95 | 3.26 | 5.43 |
| 1.29 | 0.90 0.86 0.20 | 1.15 | 1.09 | | 1.82 1.59 1.58 0.00 | 1.92 19.41 5.95 0.00 | 3.18 | 5.29 |
| 1.01 1.29 1.30 0.00 | 1.1 | 1.29 1.15 1.17 0.17 | 0.81 | 0.96 | 1.82 | 1.92 | 5.11 | 8.41 |
| 353 | 189 | 650 | 513 | 418 | 137 | 208 | 700 | 724 |

| 0.71.110 senger RNA ment for mouse recon beta ftype oding for the c- | Inal part. 0.00.317 use mRNA ment for serum loid A (SAA) 3 | tein. 0.56.075use mRNA for inal inal xynucleotidyltrain ase (TdT). | 0.21 .730use Y mosome RNA script expressed estis (bYMT2/B). | 0.00.050 640 Mouse NF- ene for middle- ecular-mass | 1.02.105use mRNA for E- herin (= morulin, = L- = cell-CAM | /80, = Arc-1). 0.00 .693 rine mRNA for c- | 0.65.078 540 Mouse c-abl | 0.74.702 rine mRNA for -1.4 protein. | 1.10.400 use mRNA for Noprotein (exons 1 | art.). 0.00 . 117 use mRNA for eticulin. |
|--|--|--|--|--|--|--|--------------------------|--------------------------------------|--|--|
| 0.82 | 0.97 | 0.99 | 0.00 | 0.00 | 0.24 | 1.95 | 0.98 | 0.00 | 0.18 | 00.00 |
| 0.00 | 0.67 | 0.04 | 1.05 | 0.00 | 0.15 | 27.29 | 0.38 | 26.77 | 0.00 | 1.17 |
| 1.18 | 1.19 | 2.45 | 0.95 | 96.9 | 0.98 | 0.016 0.00 0.05 16.10 27.29 | 1.02 | 14.07 | 0.25 | 1.17 |
| 1.63 | 0.58 | <i>0.006</i> 1.01 1.70 2.45 | 1.63 | 3.04 | 1.02 | 0.05 | 0.007 1.08 1.38 1.02 | 0.036 0.00 1.26 14.07 | 0.023 1.13 1.20 0.25 | 0.003 1.22 1.11 1.17 |
| 0.83 | 1.03 | 1.01 | 3.64 | 2.21 | 1.15 | 0.00 | 1.08 | 0.00 | 1.13 | 1.22 |
| 0.023 0.83 1.63 1.18 | <i>0.039</i> 1.03 0.58 1.19 | 0.006 | 0.011 3.64 1.63 0.95 | 0.000 2.21 | 0.007 1.15 1.02 0.98 | 0.016 | 0.007 | 0.036 | 0.023 | 0.003 |
| 0.10 | 1.17 | 0.99 | 0.00 | 0.00 | 0.17 | 00.00 | 0.47 | 0.00 | 0.90 | 926 1.00 1.00 1.56 0.00 0.00 0.00 |
| 1.17 | 0:08 | 0.37 | 1,15 1.82 2.55 0.00 0.00 0.00 | 1.17 27.06 1.14 0.00 0.00 0.00 | 1.83 1.63 1.23 0.00 0.00 | 3 83 11.36 2.49 0.00 0.00 | 0.00 | 5.05 0.26 0.00 0.00 0.00 | 2.17 1.59 0.13 0.76 | 0.00 |
| | 1.64 1.70 1.36 0.32 | 1.69 1.82 1.59 0.43 | 0.00 | 0.00 | 0.00 | 0.00 | 1.07 1.23 1.56 0.34 | 0.00 | 0.13 | 0.00 |
| 1.68 | 1.36 | 1.59 | 2.55 | 1.14 | 1.23 | 2.49 | 1.56 | 0.26 | 1.59 | 1.56 |
| 2.40 | 1.70 | 1.82 | 1.82 | 27.06 | 1.63 | 11.36 | 1.23 | | 2.17 | 1.00 |
| 2.04 2.40 1.68 0.82 | 1.64 | | | | 1.83 | 3,83 | | 7.03 | 1.47 | 1.00 |
| 755 | 479 | 123 | 260 | 640 | 115 | 368 | 540 | 538 | 664 | 926 |

| 0.96.067use mRNA for a-adaptin (C). | 1.82.956rine mRNA for roendocrine tein 782. | 0.00 . 123 use mRNA for 3.3 PRI script. | 0.00.136 usculus T | 0.00 .079 991 Mouse NA for homologue he rat T cell erentiation marker | 1.76.134 424 Mouse NA for gamma ptin | 0.00 .088 usculus mRNA CAAT-box DNA | ing protein unit A (NF-YA) | tial). 0.72.040 781 M.musculus 2 nene | 0.79.053 044 M.musculus NA for protein | 0.00 .067 349 M.musculus M. for transferrin | 0.00 . 191 usculus mRNA ribosomal protein | 1.10. <i>823</i> 876 Murine 2 mRNA for 2 protein |
|-------------------------------------|---|---|--------------------|--|--|-------------------------------------|-------------------------------|---|---|---|--|--|
| 0.00 | 0.23 | 00.00 | 0.00 | 0.00 | 0.35 | 0.00 | | 1.01 | 0.47 | 0.00 | 0.00 | 0.00 |
| 0.79 | 0.93 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | | 0.72 | 0.97 | 0.00 | 0.00 | 3.04 |
| 1.95 | 0.87 | 0.00 | 0.00 | 3.06 | 2.58 | 1.68 | | 1.13 | 1.59 | 1.98 | 0.00 | 1.04 |
| 0.003 1.99 1.04 1.95 | 1.07 | 5.28 | 32.38 | 9.53 | 2.97 | 1.85 | | 1.36 | 1.23 | 2.09 | 17.60 | 0.006 2.15 1.64 1.04 |
| 1.99 | 1.12 | 6.86 | 1.44 | 2.85 | 1.05 | 5.99 | | 0.030 1.10 1.36 | 0.019 1.10 1.23 | 6.12 | <i>0.000</i> 6.85 17.60 | 2.15 |
| 0.003 | 0.005 1.12 | 0.023 6.86 | 0.001 1,44 32.38 | 0.004 2.85 | 0.016 1.05 | 0.038 5.99 | | 0.030 | 0.019 | 0.027 6.12 | 0.000 | 0.006 |
| 0.85 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.44 | | 0.78 | 0.27 | 0.00 | 00.00 | 0.17 |
| 99.0 | 0.00 | 2.36 | 0.00 | 0.00 | 0.00 | 0.33 | | . 0.49 | 0.40 | 0.78 | 0.0 | 1.54 0.93 0.00 0.00 |
| 0.55 | 0.56 | 5.27 0.00 | 6.00 0.00 | 3.70 4.67 0.00 | 2.24 0.00 | 4.68 0.00 | | 1.53 1.53 0.06 | 0.71 | 1.22 2.82 0.00 | 0.00 | 0.00 |
| 1.66 | 1.21 0.56 | | | 4.67 | 2.24 | 4.68 | | 1.53 | 1.03 1.66 0.71 | 2.82 | 4.13 | 0.93 |
| 1.63 2.07 1.66 0.55 | 1.63 | 8.23 | 4.96 35.96 | 3.70 | 0.95 | 5.39 | | 1.53 | 1.03 | 1.22 | 1.01 56.29 4.13 0.00 | |
| 1.63 | 1.42 | 4.28 | 4.96 | 2.51 | 2.42 | 1.56 | | 0.99 | 1.26 | 2.20 | 1.01 | 96.0 |
| 972 | 830 | 510 | 683 | 991 | 424 | 315 | | 781 | 044 | 349 | 096 | 876 |

÷

| 1.06.160use mRNA for a wth factor- cible immediate y gene (3CH134). | 0.10.108 285 M.musculus for HC1 locus | 2,12,558 449 M.musculus NA for calcyclin | 0.00.117 usculus VCAM-1 NA. | 0.65.093 usculus HCNGP NA. | 0.00 . 161 usculus mRNA inhibin beta-B | 2.28.775 018 M.musculus NA for Id4 helix- | ti.06.939 295 M.niusculus e for | anocortin 5 | 0.00.352 usculus cadL NA. | 0.00 .889 304 M. culus (SRP9) | al recognition icle subunit NA. 689bp | 1.30.382 usculus Six1 NA. | 1.70. <i>507</i> usculus KIS NA. | 0.93. <i>685</i> usculus mRNA K-glypican. | 1.09. <i>101</i> usculus PTX3 NA. |
|--|---------------------------------------|---|--------------------------------|-------------------------------|--|--|---------------------------------|-------------|------------------------------|----------------------------------|---|------------------------------|-------------------------------------|--|--------------------------------------|
| 1.15 | 1.18 | 0.00 | 0.00 | 0.29 | 0.00 | 0.75 | 1.57 | | 0.00 | 1.36 | | 0.19 | 0.33 | 0.99 | 0.74 |
| 0.99 | 0.00 | 0.00 | 0.00 | 0.98 | 0.00 | 0.85 | 0.58 | | 1.06 | 1.25 | | 0.29 | 0.51. | 2.09 | 0.22 |
| 1.66 | 0.82 | 0.64 | 0.00 | 1.02 | 00.0 | 0.72 | 1.28 | | 3.07 | 1.57 | | 0.00 | 0.85 | 1.33 | 1.20 |
| 1.55 | 2.00 | 1.36 | 3.70 | 1.08 | 34.28 | 1.39 | 0.69 | | 1.04 | 0.040 0.08 1.25 1.57 | | 1.98 | 1.58 | 1.06 | 0.006 1.21 1.25 1.20 |
| 1.03 | 1.64 | 1.58 | 3.31 | 1.55 | 6.71 | 1.27 | 1.17 | | 0.00 | 0.08 | | 2.01 | 1.15 | 1.12 | 1.21 |
| <i>0.003</i> 1.03 1.55 1.66 | 0.000 1.64 | 0.000 1.58 | 0.003 | 0.001 1.55 | 0.000 6.71 34.28 | 0.024 1.27 1.39 | 71.1 610.0 | | 0.026 0.00 | 0.040 | | 0.003 2.01 | 0.009 1.15 | 0.049 1.12 | 0.006 |
| 0.19 | 0.00 | 0.00 | 1.53 | 0.56 | 0.00 | 0.87 | 0.65 | | 0.00 | 0.00 | | 0.70 | 0.39 | 0.75 | 0.42 |
| 0.24 | 00.00 00.00 | 0.00 | 0.0 | 0.41 | 0.00 | 0.53 | 0.24 | | 0.00 | 0.00 | | 0.31 | 0.00 | 0.28 | 1.37 0.91 0.00 0.20 |
| | | | 0.47 | 0.74 | 0.00 | 0.29 | 0.00 | | 96.0 | 99.0 | | 1.68 1.68 0.00 | 0.73 | 0.48 | 0.00 |
| 0.80 | 1.92 | 1.43 | 4.48 | 1.45 | 3.86 0.00 | 1.17 | 1.01 | | 2.37 1.37 0.96 | 0.75 0.66 | | 1.68 | 1.81 1.76 0.73 | 1.01 0.81 0.48 | 0.91 |
| 0.88 0.80 0.43 | 1.96 1.92 0.00 | 1.75 1.43 0.00 | 3.48 4.48 0.47 | 1.51 | 2.94 | 1.13 1.17 0.29 | 1.24 1.01 0.00 | | 2.37 | 1.67 | | 1.68 | 1.81 | 1.01 | 1.37 |
| 940 1.01 | 2.49 | | 4.50 | 1.34 | 4.60 22.94 | 1.41 | 0.99 | | 1.74 | 1.82 | | 1.68 | | 1.23 | 1.16 |
| 940 | 285 | 449 | 783 | 061 | 620 | 018 | 295 | | 557 | 304 | | 339 | 320 | 577 | 601 |

| 0.33.092 usculus mRNA ryanodine | 0.00 .131 usculus putative scription factor. | 0.96. <i>053 usculus</i> mRNA Bpx protein. | 1.10.103 664 M.musculus NA for ubiquitin | jugating enzyine M2 0.00 .131 usculus mRNA Ott protein, clone 7. | 1.02.079 719 M.musculus ovirus restriction | e FV I 0.18 .071 817 M.musculus NA for | aphorin F 1.65.511 581 M.musculus gene encoding ocyte-dervied seven smembrane domain receptor. | 5.00 .379use glandular ikrein gene. | 0.00 .310use int-2 gene. 1.03 .330 usculus miRNA 5HT1E bete | tonin receptor. 0.61. <i>085</i> usculus Mox-1 NA. | 1.07 .099 usculus ALK-6 NA, complete | 0.00 .418 usculus mRNA follistatin. |
|------------------------------------|--|---|---|--|---|--|--|--|---|--|---|--|
| 0.64 | 0.00 | 0.28 | 0.42 | 0.82 | 0.00 | 0.00 | 0.00 | 1.13 | 0.75 | 1.08 | 0.16 | 0.90 |
| 1.12 | 00.00 | 0.64 | 0.00 | 0.97 | 0.51 | 1.04 | 0.91 | 0.53 | 1.25 | 0.54 | 0.01 | 1.10 |
| 1.88 | 54.33 | 1.24 | 0.91 | 2.07 | 1.47 | . 0.96 | 1.36 | 0.63 | 2.96 0.97 | 1.18 | 0.93 | 0.65 |
| 0.93 | 36.57 | 1.05 | 1.46 | 1.20 | 0.98 | 1.65 | | 1.06 | 0.00 | 1.16 | 1.71 | 1.29 |
| 2.12 | 0.00 | 1.47 | 1.51 | 1.03 | 1.98 | 1.39 | 1.09 | 0.79 | 2.48 | 1.07 | 1.20 | 1.11 |
| 0.010 2.12 | 0.007 0.00 36.57 54.33 | 0.000 1.47 | 0.033 1.51 | 0.000 1.03 | 0.025 1.98 | 0.005 1.39 | 0.007 1.09 1.15 | 0.044 0.79 | 0.001 2.48 0.011 1.18 | 0.003 1.07 | 0.007 1.20 | 0.000 1.11 1.29 0.65 |
| 0.38 | 0.00 | 0.32 | 0.17 | 0.00 | 99.0 | 0.27 | 0.14 | 0.21 | 0.03 | 0.28 | 0.54 | 0.00 |
| 0.34 | 0.00 | 0.35 | 0.70 | 0.00 | 0.00 | 0.00 | 0.00 | 0.34 | 0.00 | 1.40 1.05 0.24 0.19 | 0.67 | 0.00 |
| | | 0.10 | 0.82 | | 0.59 | | 0.10 | 0.94 | 5.83 0.00 1.37 0.00 | 0.24 | 0.15 | 0.00 |
| 1.07 | 0.0 | 1.17 | 1.09 | 1.31 | 1.15 | 1.57 | 1.18 | 1.10 | 5.83 1.37 | 1.05 | 1.28 | 1.27 |
| 1.54 1.19 1.07 0.66 | 5.46 35.26 0.09 0.00 | 1.19 1.26 1.17 0.10 | 1.32 1.29 1.09 0.82 | 1.33 1.60 1.31 0.00 | 1.64 1.19 1.15 0.59 | 1.16 1.42 1.57 0.55 | 1,13 0.64 1.18 0.10 | 1.36 1.92 1.10 0.94 | 4.44 5.83 0.00 1.18 1.37 0.00 | | 1.38 1.28 0.15 | 1.23 1.37 1.27 0.00 0.00 |
| 1.54 | 5.46 | 1.19 | 1.32 | 1.33 | 1.64 | 1.16 | 1.13 | 1.36 | 6.67 | 0.95 | 1.19 | 1.23 |
| 932 | 368 | 352 | 664 | 909 | 719 | 817 | 581 | 200 | 848 224 | 103 | 143 | 532 |

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| 0.56.544 166 M.musculus Ib/c) mRNA for agen IV alpha 3 | 1.12 0.77.728 168 M.musculus NA for collagen | Ipna 5 cnain 4 1.02 .639 147 M.musculus e for cell esion regulator | | | | |
|--|---|--|--|--|--|--|
| 0.00 | 1.1 | 0.0 | | | | |
| 2.29 | 0.55 | 1.17 | | | | |
| 1.05 | 1.00 | 0.66 1.18 | | | | |
| 1.51 | 1.68 | 0.66 | | | | |
| 1.71 | 1.26 | 0.98 | | | | |
| 0.002 1.71 1.51 1.05 | 0.041 1.26 1.68 1.00 | 0.001 | | | | |
| 0.26 | 90.0 | 0.00 70 | | | | |
| 0.00 | 0.82 | 0.07 | | | | |
| 0.00 | 0.05 | 0.00 | | | | |
| 1.34 | 1.05 | 1.08 | | | | |
| 1.35 | 1.35 | 1.63 | | | | |
| 0.95 1.35 1.34 0.00 0.00 | 168 1.00 1.35 1.05 0.05 0.82 0.06 | 147 1.42 1.63 1.08 0.00 0.07 | | | | |
| 166 | 168 | 147 | | | | |
| | | | | | | |